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   * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * *


 *ENCOMPPAT     - EnCompass Patent File 1964-present (Supporters)
 *ENCOMPPAT2    - EnCompass Patent File 1964-Present (Non-Supporters)

   * The files listed above are temporarily unavailable.

 FILE 'HOME' ENTERED AT 08:46:09 ON 15 DEC 2003

 => fil .bec
 COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
 FULL ESTIMATED COST                                        0.21       0.21

 FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,
        ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 08:46:34 ON 15 DEC 2003
 ALL COPYRIGHTS AND RESTRICTIONS APPLY.  SEE HELP USAGETERMS FOR DETAILS.

 11 FILES IN THE FILE LIST

 => s arginine methyltransferase#
 FILE 'MEDLINE'
          59763 ARGININE
          14615 METHYLTRANSFERASE#
 L1          98 ARGININE METHYLTRANSFERASE#
                  (ARGININE(W)METHYLTRANSFERASE#)

 FILE 'SCISEARCH'
          51624 ARGININE
          11088 METHYLTRANSFERASE#
 L2         111 ARGININE METHYLTRANSFERASE#
                  (ARGININE(W)METHYLTRANSFERASE#)

 FILE 'LIFESCI'
          14117 "ARGININE"
           4253 METHYLTRANSFERASE#
 L3          55 ARGININE METHYLTRANSFERASE#
                  ("ARGININE"(W)METHYLTRANSFERASE#)

 FILE 'BIOTECHDS'
           1774 ARGININE
            584 METHYLTRANSFERASE#
 L4           5 ARGININE METHYLTRANSFERASE#
                  (ARGININE(W)METHYLTRANSFERASE#)

 FILE 'BIOSIS'
          71049 ARGININE
          12065 METHYLTRANSFERASE#
 L5         101 ARGININE METHYLTRANSFERASE#
                  (ARGININE(W)METHYLTRANSFERASE#)

 FILE 'EMBASE'
          54906 "ARGININE"
          11378 METHYLTRANSFERASE#
 L6         117 ARGININE METHYLTRANSFERASE#
                  ("ARGININE"(W)METHYLTRANSFERASE#)

 FILE 'HCAPLUS'
          97624 ARGININE
          13953 METHYLTRANSFERASE#
 L7         158 ARGININE METHYLTRANSFERASE#
                  (ARGININE(W)METHYLTRANSFERASE#)
```

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FILE 'NTIS'
           295 ARGININE
            47 METHYLTRANSFERASE#
L8           1 ARGININE METHYLTRANSFERASE#
                 (ARGININE(W)METHYLTRANSFERASE#)

FILE 'ESBIOBASE'
         21483 ARGININE
          4024 METHYLTRANSFERASE#
L9          69 ARGININE METHYLTRANSFERASE#
                 (ARGININE(W)METHYLTRANSFERASE#)

FILE 'BIOTECHNO'
         17707 ARGININE
          5433 METHYLTRANSFERASE#
L10         81 ARGININE METHYLTRANSFERASE#
                 (ARGININE(W)METHYLTRANSFERASE#)

FILE 'WPIDS'
          5647 ARGININE
           386 METHYLTRANSFERASE#
L11          6 ARGININE METHYLTRANSFERASE#
                 (ARGININE(W)METHYLTRANSFERASE#)

TOTAL FOR ALL FILES
L12        802 ARGININE METHYLTRANSFERASE#

=> s l12 and (gene/q or mouse or murine)
FILE 'MEDLINE'
        247783 MOUSE
        106494 MURINE
L13         73 L1 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'SCISEARCH'
        268802 MOUSE
        110272 MURINE
L14         73 L2 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'LIFESCI'
         99327 MOUSE
         47548 MURINE
L15         38 L3 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHDS'
         24676 MOUSE
          2889 MURINE
L16          4 L4 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOSIS'
        694272 MOUSE
        141630 MURINE
L17         65 L5 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'EMBASE'
        534665 MOUSE
         95892 MURINE
L18         82 L6 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'HCAPLUS'
        289658 MOUSE
         96510 MURINE
L19        104 L7 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'NTIS'
```

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          4021 MOUSE
           922 MURINE
L20          1 L8 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'ESBIOBASE'
         89960 MOUSE
         39213 MURINE
L21         45 L9 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHNO'
        223726 MOUSE
         55611 MURINE
L22         63 L10 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'WPIDS'
         20982 MOUSE
          3361 MURINE
L23          4 L11 AND (GENE/Q OR MOUSE OR MURINE)

TOTAL FOR ALL FILES
L24        552 L12 AND (GENE/Q OR MOUSE OR MURINE)

=> s (steroid or glucocorticoid)(w)receptor#
FILE 'MEDLINE'
         74869 STEROID
         22775 GLUCOCORTICOID
        621640 RECEPTOR#
L25      10538 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'SCISEARCH'
         56143 STEROID
         23725 GLUCOCORTICOID
        663557 RECEPTOR#
L26      14018 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'LIFESCI'
         11870 STEROID
          5755 GLUCOCORTICOID
        203748 RECEPTOR#
L27       3308 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'BIOTECHDS'
          2467 STEROID
           336 GLUCOCORTICOID
         14659 RECEPTOR#
L28         201 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'BIOSIS'
         83643 STEROID
         27852 GLUCOCORTICOID
        733241 RECEPTOR#
L29      12599 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'EMBASE'
         95685 STEROID
         34861 GLUCOCORTICOID
        695788 RECEPTOR#
L30      12476 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'HCAPLUS'
         99850 STEROID
         25645 GLUCOCORTICOID
        638987 RECEPTOR#
L31      13532 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#
```

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FILE 'NTIS'
           620 STEROID
           108 GLUCOCORTICOID
          6167 RECEPTOR#
L32         91 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'ESBIOBASE'
         19300 STEROID
          7478 GLUCOCORTICOID
        248617 RECEPTOR#
L33       4304 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'BIOTECHNO'
         19297 STEROID
          9459 GLUCOCORTICOID
        210907 RECEPTOR#
L34       5480 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

FILE 'WPIDS'
          7630 STEROID
          1219 GLUCOCORTICOID
         40157 RECEPTOR#
L35        387 (STEROID OR GLUCOCORTICOID)(W)RECEPTOR#

TOTAL FOR ALL FILES
L36      76934 (STEROID OR GLUCOCORTICOID)(W) RECEPTOR#

=> s transcription?(10a)(activat? or coactivat?)
FILE 'MEDLINE'
        232295 TRANSCRIPTION?
        634692 ACTIVAT?
          3655 COACTIVAT?
L37      35832 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'SCISEARCH'
        204348 TRANSCRIPTION?
        697917 ACTIVAT?
          4972 COACTIVAT?
L38      41690 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'LIFESCI'
        105848 TRANSCRIPTION?
        203495 ACTIVAT?
          2048 COACTIVAT?
L39      23706 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHDS'
         15419 TRANSCRIPTION?
         22144 ACTIVAT?
            56 COACTIVAT?
L40       1373 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'BIOSIS'
        234995 TRANSCRIPTION?
        659287 ACTIVAT?
          3853 COACTIVAT?
L41      41261 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'EMBASE'
        206063 TRANSCRIPTION?
        559602 ACTIVAT?
          3440 COACTIVAT?
L42      33523 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)
```

```
FILE 'HCAPLUS'
       266897 TRANSCRIPTION?
      1088189 ACTIVAT?
         4394 COACTIVAT?
L43      55447 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'NTIS'
         2456 TRANSCRIPTION?
        27676 ACTIVAT?
          100 COACTIVAT?
L44         260 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'ESBIOBASE'
       119781 TRANSCRIPTION?
       254595 ACTIVAT?
         2786 COACTIVAT?
L45      25879 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHNO'
       170452 TRANSCRIPTION?
       230606 ACTIVAT?
         2255 COACTIVAT?
L46      26724 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'WPIDS'
        12390 TRANSCRIPTION?
       228964 ACTIVAT?
          279 COACTIVAT?
L47       1360 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

TOTAL FOR ALL FILES
L48     287055 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

=> s (l36 or l48)(10a)methyltransferase#
FILE 'MEDLINE'
        14615 METHYLTRANSFERASE#
L49        27 (L25 OR L37)(10A)METHYLTRANSFERASE#

FILE 'SCISEARCH'
        11088 METHYLTRANSFERASE#
L50        35 (L26 OR L38)(10A)METHYLTRANSFERASE#

FILE 'LIFESCI'
         4253 METHYLTRANSFERASE#
L51        27 (L27 OR L39)(10A)METHYLTRANSFERASE#

FILE 'BIOTECHDS'
          584 METHYLTRANSFERASE#
L52         4 (L28 OR L40)(10A)METHYLTRANSFERASE#

FILE 'BIOSIS'
        12065 METHYLTRANSFERASE#
L53        33 (L29 OR L41)(10A)METHYLTRANSFERASE#

FILE 'EMBASE'
        11378 METHYLTRANSFERASE#
L54        33 (L30 OR L42)(10A)METHYLTRANSFERASE#

FILE 'HCAPLUS'
        13953 METHYLTRANSFERASE#
L55        83 (L31 OR L43)(10A)METHYLTRANSFERASE#

FILE 'NTIS'
```

```
            47 METHYLTRANSFERASE#
L56          0 (L32 OR L44)(10A)METHYLTRANSFERASE#

FILE 'ESBIOBASE'
          4024 METHYLTRANSFERASE#
L57         25 (L33 OR L45)(10A)METHYLTRANSFERASE#

FILE 'BIOTECHNO'
          5433 METHYLTRANSFERASE#
L58         21 (L34 OR L46)(10A)METHYLTRANSFERASE#

FILE 'WPIDS'
           386 METHYLTRANSFERASE#
L59          3 (L35 OR L47)(10A)METHYLTRANSFERASE#

TOTAL FOR ALL FILES
L60        291 (L36 OR L48)(10A) METHYLTRANSFERASE#

=> s (l24 or l60) not 2000-2003/py
FILE 'MEDLINE'
       2011683 2000-2003/PY
L61         29 (L13 OR L49) NOT 2000-2003/PY

FILE 'SCISEARCH'
       3887743 2000-2003/PY
L62         35 (L14 OR L50) NOT 2000-2003/PY

FILE 'LIFESCI'
        387284 2000-2003/PY
L63         24 (L15 OR L51) NOT 2000-2003/PY

FILE 'BIOTECHDS'
         75267 2000-2003/PY
L64          0 (L16 OR L52) NOT 2000-2003/PY

FILE 'BIOSIS'
       2099866 2000-2003/PY
L65         32 (L17 OR L53) NOT 2000-2003/PY

FILE 'EMBASE'
       1749601 2000-2003/PY
L66         39 (L18 OR L54) NOT 2000-2003/PY

FILE 'HCAPLUS'
       3827495 2000-2003/PY
L67         44 (L19 OR L55) NOT 2000-2003/PY

FILE 'NTIS'
         62673 2000-2003/PY
L68          0 (L20 OR L56) NOT 2000-2003/PY

FILE 'ESBIOBASE'
       1113581 2000-2003/PY
L69         16 (L21 OR L57) NOT 2000-2003/PY

FILE 'BIOTECHNO'
        477989 2000-2003/PY
L70         22 (L22 OR L58) NOT 2000-2003/PY

FILE 'WPIDS'
       3461185 2000-2003/PY
L71          0 (L23 OR L59) NOT 2000-2003/PY

TOTAL FOR ALL FILES
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L72 241 (L24 OR L60) NOT 2000-2003/PY

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	15.27	15.48

STN INTERNATIONAL LOGOFF AT 08:51:16 ON 15 DEC 2003

	L #	Hits	Search Text	DBs	Time Stamp
1	L1	25	arginine adj methyltransferase$1	USPAT; US-PGPUB	2003/12/15 08:32
2	L2	2570	(steroid or glucocorticoid) adj receptor$1	USPAT; US-PGPUB	2003/12/15 08:32
3	L3	15188	transcription$ near6 (activat$8 or coactivat$8)	USPAT; US-PGPUB	2003/12/15 08:32
4	L4	96	(2 or 3) same methyltransferase$1	USPAT; US-PGPUB	2003/12/15 08:33
5	L5	114	1 or 4	USPAT; US-PGPUB	2003/12/15 08:33

PGPUB-DOCUMENT-NUMBER: 20030224040

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030224040 A1

TITLE: Genomic screen for epigenetically silenced genes associated with cancer

PUBLICATION-DATE: December 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Baylin, Stephen B.	Baltimore	MD	US	
Herman, James	Lutherville	MD	US	
Suzuki, Hiromu	Baltimore	MD	US	

APPL-NO: 10/ 384491

DATE FILED: March 7, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60362422 20020307 US

US-CL-CURRENT: 424/450, 435/6 , 514/44

ABSTRACT:

A method of identifying epigenetically silenced genes, e.g., methylation silenced genes, in cancer cells is provided. In addition, methods of identifying a cancer by detecting epigenetic silencing of gene expression are provided, as are methods of treating a subject having such a cancer, for example, a colorectal cancer and/or gastric cancer. Reagents for practicing such methods also are provided.

[0001] This application claims the benefit of priority under 35 U.S.C. .sctn. 119(e)(1) of U.S. Ser. No. 60/362,422, filed Mar. 7, 2002, the entire content of which is incorporated herein by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (123):

[0160] From the standpoint of transcriptionally repressive chromatin, the disclosed strategy has provided important information about the promoters of genes with various responses to the inhibitors utilized. The results for Group la genes confirmed that densely methylated genes will not re-express if exposed to HDAC inhibition alone. In contrast, the results for Group 2 genes revealed that those genes that do re-express or up-regulate expression following HDAC

inhibition, alone, have a lack of promoter methylation, even when CpG islands were present in their 5' regions. The present study discloses genes that were up-regulated after treatment of cells with the demethylating agent, DAC, even though the promoters of these genes were unmethylated. Similar findings were previously reported (Soengas et al., Nature 409, 207-211 (2001). While methylation of upstream genes, such as **transcription factors, could secondarily result in activation** of these genes, another possibility is that inhibitors of DNA **methyltransferases** (DNMTs), such as DAC, affect these proteins other than by blocking their methylating capacities. Recent studies revealed that DNMTs have the potential directly, and through interaction with HDACs and other corepressor proteins, to repress transcription independently of their methylating activities (Rountree et al., Nature Genet. 25:269-277, 2000; Bachman et al., J. Biol. Chem. 276:32282-32287, 2001; Fuks et al., Nature Genet. 24:88-91, 2000; Fuks et al., EMBO J. 20:2536-2544, 2001; Robertson et al. Nature Genet. 25:338-342, 2000).

PGPUB-DOCUMENT-NUMBER: 20030198981

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030198981 A1

TITLE: Genes and proteins involved in the biosynthesis of lipopeptides

PUBLICATION-DATE: October 23, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Farnet, Chris M.	Outremont		CA	
Staffa, Alfredo	Saint-Laurent		CA	
Zazopoulos, Emmanuel	Montreal		CA	

APPL-NO: 10/ 329079

DATE FILED: December 24, 2002

RELATED-US-APPL-DATA:

child 10329079 A1 20021224

parent continuation-in-part-of 10232370 20020903 US PENDING

non-provisional-of-provisional 60342133 20011226 US

non-provisional-of-provisional 60372789 20020417 US

US-CL-CURRENT: 435/6, 435/219 , 435/252.3 , 435/320.1 , 435/69.1 , 536/23.2

ABSTRACT:

Genes and proteins involved in the biosynthesis of lipopeptides by microorganisms, in particular the nucleic acids forming the biosynthetic locus for the A54145 lipopeptide from Streptomyces fradiae and the A54145-like lipopeptide from Streptomyces refuineus. These nucleic acids can be used to make expression constructs and transformed host cells for the production of lipopeptides. The genes and proteins allow direct manipulation of lipopeptides and related chemical structures via chemical engineering of the proteins involved in the biosynthesis of A54145.

CROSS-REFERENCING TO RELATED APPLICATION

[0001] This application claims benefit of provisional application U.S. S No. 60/342,133, filed on Dec. 26, 2001 and of U.S. S No. 60/372,789, filed on Apr. 17, 2002. The application is also a continuation-in-part of U.S. Ser. No. 10/232,370, filed on Sep. 3, 2002. The teachings of the above applications are hereby incorporated by reference in their entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (137):

[0172] A search of the NCBI gene database identified a homologue with 35% identity to ORF 15 in Streptomyces coelicolor A3(2), hypothetical protein SCE8.08c (GenBank accession CAB38586). Further inspection of the genetic context of the gene encoding SCE8.08c revealed that it is located approximately 20 kilobasepairs upstream of the NRPS genes that are responsible for the production of the "calcium-dependent antibiotic" (CADA) of S. coelicolor and less than 3.5 kilobasepairs upstream of the gene encoding the CdaR **transcriptional activator** protein for CADA biosynthesis. CADA is an example of an N-acylated lipopeptide and, significantly, it too varies at one position of the peptide core in that either glutamate or 3-methyl-glutamate is found in the 10.sup.th position of the eleven amino acid core. In an elegant study using microarray expression profile analysis, Huang and coworkers recently demonstrated that the gene encoding hypothetical protein SCE8.08c is among those that are expressed coordinately along with the CADA NRPS cluster (Huang et al. (2001) Genes Dev. Vol. 15 pp. 3183-3192). This finding supports our hypothesis implicating hypothetical protein SCE8.08c in the formation of 3-methyl-glutamate-containing CADA compounds. In contrast to the function which we propose here for hypothetical protein SCE8.08c, Ryding and coworkers have recently suggested that it is involved in the synthesis of tryptophan, a precursor used in the biosynthesis of CADA which is incorporated at both the third and eleventh positions. Their conclusion was based merely on the fact that the SCE8.08c gene is one of the six genes, most of which are homologues of known tryptophan biosynthetic genes, that is expressed as an operon transcribed from a single promoter known as p7 (Ryding (2002) J. Bact. Vol. 184 pp. 794-805). We disagree with these authors' proposed function for SCE8.08c as no C**-methyltransferase** is required in the tryptophan biosynthetic pathway.

PGPUB-DOCUMENT-NUMBER: 20030194764

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030194764 A1

TITLE: Compositions and methods for the therapy and diagnosis of lung cancer

PUBLICATION-DATE: October 16, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Bangur, Chaitanya S.	Seattle	WA	US	
Switzer, Ann	Seattle	WA	US	

APPL-NO: 10/ 116712

DATE FILED: April 4, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60327511 20011005 US

non-provisional-of-provisional 60282289 20010405 US

US-CL-CURRENT: 435/69.1, 435/183 , 435/320.1 , 435/325 , 530/350 , 536/23.1

ABSTRACT:

Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

---------- KWIC ---------

Detail Description Table CWU - DETL (2):

3TABLE 3 Mean Signal 1/ Mean Signal Mean Signal Mean Signal 2 1 (Tumor 2 (Normal humanES SEQ ID # Clone ID # Ratio Group) Tissues) GenBank Match T < 1e - 25 1 61571741 3.76 0.155 0.041 cDNA: FLJ23386 fis (AK027039) 12 2 61571742 2.35 0.165 0.07 topoisomerase II alpha (TOP2A) 35 4 61571744 6.03 0.286 0.047 DEK oncogene (NM_003472) 75 7 61571747 3.19 0.177 0.055 KIAA1563 protein, partial cds 7 (AB046783) 11 61571753 3.16 0.223 0.07 cDNA FLJ12780 fis (AK022842) 7 12 61571754 3.69 0.14 0.038 calcium/calmodulin-dependent 20 serine protein kinase (CASK)(AF035582) 15 61571758 3.56 0.313 0.088

Chromosome 12q 13.1 101 (AC004801) 17 61571760 3.59 0.194 0.054 ALEX3 protein (NM_016607) 27 18 61571761 3.82 0.14 0.037 MTG8-like protein: MTGR1a 47 (AF069747); MTGR1b (AF013970) 20 61571763 4.35 0.118 0.027 deoxyguanosine kinase (U41668) 101 21 61571764 2.24 0.151 0.068 KDEL (Lys-Asp-Glu-Leu) 112 endoplasmic reticulum protein retention receptor 1 (NM_006801) 25 61571768 3.53 0.244 0.069 CDNA: FLJ23494 fis (AK027147) 8 26 61571770 3.17 0.197 0.062 chromosome 9p11-13.3 7 (AL135785) 30 61571774 4.91 0.158 0.032 divalent cation tolerant protein 33 (AF106943) 31 61571775 2.64 0.107 0.04 thymopoietin 33 33 61571778 4.66 0.137 0.029 tousled-like kinase 2 (TLK2) 33 (AF162667) 34 61571780 2.26 0.191 0.084 apobec-1 binding protein 1 65 (U76713) 36 61571782 34.23 0.135 0.004 DNA polymerase zeta catalytic 19 subunit (AF179429) 38 61571786 8.12 0.18 0.022 proliferating cell nuclear antigen 140 (PCNA) 41 61571789 2.83 0.123 0.043 protein phosphatase 1B 20 (NM_002706) 42 61571790 2.15 0.167 0.078 cDNA: FLJ21925 fis (AK025578) 17 46 61571795 2.3 0.104 0.045 thyroid hormone receptor- 9 associated protein complex TRAP170 (AF135802) 53 61571804 2.81 0.128 0.045 mRNA export protein (RAE1) 109 (U84720) 57 61571808 3.04 0.226 0.075 K1AA0878 protein (XM_004037) 40 59 61571811 2.35 0.195 0.083 cDNA: FLJ21925 fis (AK025578) 21 65 61571819 5.64 0.145 0.026 chromosome X (AL050310) 0 70 61571824 2.25 0.209 0.093 DKFZP434A043 protein 58 (XM_003112) 71 61571825 3.34 0.142 0.042 cDNA DKFZp434N2O72 70 (AL133580) 72 61571826 2.75 0.11 0.04 cyclin B (M25753) 42 73 61571827 3.93 0.133 0.034 KIAA0840 protein (AB020647) 53 74 61571828 10.56 0.111 0.01 dynamin 2 (NM_004945); nt1-85 30 75 61571829 3.29 0.165 0.05 chromosome 9p11-13.3 7 (AL135785) 77 61571831 2.26 0.155 0.068 phosphoglycerate dehydrogenase 143 79 61571833 2.08 0.187 0.09 clone H17 unknown mRNA 43 (AF103801) 83 61483101 14.06 0.114 0.008 chromosome 9 (AL161628) 1 85 61483103 21.35 0.192 0.009 Mus musculus neuronal 1 differentiation related protein (AB049460) 86 61483104 8.23 0.18 0.022 ubiquitin-conjugating enzyme E2 80 (AF160215) 87 61483107 3.51 0.112 0.032 divalent cation tolerant protein 33 CUTA 88 61483108 2.83 0.155 0.055 myosin regulatory light chain 16 interacting protein (NM_013262) 90 61483110 2.48 0.187 0.076 serine/threonine-protein kinase 19 PRP4 homolog (XM_004079) 92 61483112 8.1 0.23 0.028 trinucleotide repeat DNA binding 14 protein p20-CGGBP (AF094481) 94 61483114 2.08 0.109 0.052 DNA (cytosine-5)- 17 **methyltransferase** 1 (NM_001379) 96 61483116 2.82 0.136 0.048 DNA (cytosine-5)- 17 **methyltransferase** 1 (NM_001379) 97 61483117 9.45 0.132 0.014 GOP dissociation inhibitor 1 63 (NM_001493) 99 61483119 2.85 0.179 0.063 KIAA0372 gene product 54 (NM_014639) 102 61483122 4.44 0.11 0.025 Cdc7-related kinase 15 108 61483129 7.38 0.122 0.016 K1AA1477 protein (AB040910) 6 109 61483130 7.1 0.143 0.02 short stature homeobox 2 0 (SHOX2), transcript variant SHOX2a (NM)_006884); SHOX2b (NM_003030) 110 61483132 7.43 0.166 0.022 chromosome Xq28 (AF003626) 23 111 61483133 5.83 0.143 0.024 protein tyrosine phosphatase, 28 receptor type, U (NM_005704) 112 61483134 2.29 0.107 0.047 chromosome 9p11-13.3 7 (AL135785) 114 61483136 2.32 0.242 0.104 Bcl-2-interacting protein beclin 62 (AF077301) 116 61483138 10.26 0.18 0.018 KIAA0169 protein (D79991) 29 117 61483140 7.34 0.115 0.016 chromosome 9p11-13.3 7 (AL135785) 124 61483147 2 0.118 0.059 phosphomannomutase 1 72 (XM_010019) 126 61483150 11.13 0.109 0.01 G-substrate (AF097730) 9 127 61483151 10.63 0.101 0.01 chromosome 1q24.1-25.3 3 (AL355520) 131 61483155 5.15 0.116 0.022 TRAF4 associated factor 1 26 (U81002) 135 61483160 3.97 0.268 0.068 cyclin B2 75 136 61483161 3.7 0.148 0.04 KIAA1171 protein (AB032997) 18 138 61483164 2.63 0.121 0.046 hypothetical protein FLJ13222 19 (NM_021943) 140 61483167 6.43 0.123 0.019 corticotropin releasing hormone- 6

binding protein (NM_001882) 141 61483168 2.85 0.138 0.048 DNA (cytosine-5-)-
19 **methyltransferase** 1 (NM_001379) 144 61483172 2.58 0.179 0.069
microtuble-associated protein 1B 10 (NM_005909) 148 61483176 2.59 0.274
0.106 Hfb1 protein, 3'UTR (Y15167) 18 149 61483177 2.59 0.151 0.058
proliferating cell nuclear antigen 107 (PCNA) 151 61483179 2.45 0.268 0.109
cDNA DKFZp586L081 18 (AL080234) 152 61483180 2.26 0.147 0.065 phosphoribosyl
phyrophosphate 1 synthetase 2 (NM_002765) 153 61483182 17.65 0.102 0.006
threonyl-tRNA synthetase 18 156 61483185 9.22 0.136 0.015 chromosome 9
(AL161628) 37 160 61483189 3.09 0.136 0.044 cDNA: FLJ22351 fis (AK026004) 5
161 61483190 27.29 0.112 0.004 calcium/calmodulin-dependent 66 serine protein
kinase (CASK)(AF035582) 165 61594545 5.95 0.198 0.033 cDNA FLJ12947 fis
(AK023009) 20 167 61594547 6.01 0.106 0.018 deoxyhypusine synthase 52
(U40579) 172 61594553 8.87 0.175 0.02 neurogenic differentiation 1 17
(NeuroD)(NM_002500) 177 61594558 2.07 0.18 0.087 beta-**glucocorticoid receptor**
0 (X03348, M11050) 179 61594560 3.15 0.165 0.052 chromosome 5 (AC010457) 65
184 61594565 2.39 0.137 0.057 KIAA0826 protein (AB020633) 46 191 61594574
2.59 0.139 0.054 topoisomerase-related function 13 protein 4 (NM_006999) 193
61594576 7.11 0.258 0.036 kinesin family member 4A 16 (KIF4A), (NM_012310)
196 61594579 3.22 0.409 0.127 nuclear autoantigenic sperm 13 protein
(histone-binding); (NM_002482) 197 61594582 5.16 0.256 0.05 cDNA
DKFZp761A07121 104 (AL161957) 199 61594583 3.47 0.167 0.048 U6
snRNA-associated Sm-like 12 protein LSm7 (AF182293) 200 61594584 2.9 0.373
0.129 PTD011 protein (NM_014051) 67 201 61594585 2.89 0.195 0.067 KIAA0826
protein (AB020633) 81 202 61594586 4.62 0.106 0.023 G-substrate (AF097730) 13
204 61594589 2.57 0.135 0.052 14-3-3 protein epsilon isoform 9 (U20972) 206
61594592 2.31 0.188 0.081 nucleolar protein hNop56 133 (Y12065) 210 61594596
2.39 0.161 0.067 cDNA: FLJ22044 fis (AK025697) 70 212 61594601 3.17 0.105
0.033 Chromosome 12q22 (AC007298) 16 214 61594604 2.45 0.293 0.12
uncharacterized bone marrow 3 protein BM036 (AF217512) 218 61594611 2.41
0.168 0.07 KIAA0038 (D26068) 5 226 61S94620 3.72 0.192 0.052 chromosome 9
(AL161628) 127 227 61594621 2.22 0.15 0.068 KIAA0850 protein (AB020657) 5
230 61594625 2.64 0.113 0.043 kappa opioid receptor (U11053) 21 236 61594632
3.78 0.13 0.034 NB thymosin beta 2 239 61571929 2.58 0.111 0.043 KIAA1499
protein (AB040932) 25 242 61571932 2.23 0.146 0.065 protein tyrosine
phosphatase,18 receptor type, U (NM_005704) 249 61571941 6.78 0.141 0.021
microtuble-associated protein-2 28 (U32996) 251 61571943 4.16 0.154 0.037
cDNA: FLJ21971 fis (AK025624) 17 253 61571946 3.58 0.122 0.034 chromosome 20
(AL121752) 52 254 61571947 2.21 0.233 0.105

PGPUB-DOCUMENT-NUMBER: 20030180927

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030180927 A1

TITLE: Yeast protein methyltransferase hsl7p

PUBLICATION-DATE: September 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Pestka, Sidney	North Caldwell	NJ	US	
Cook, Jeffry R.	Kendall Park	NJ	US	
Kinzy, Terri Goss	Bridgewater	NJ	US	
Lee, Jin-Hyung	Piscataway	NJ	US	
Norris, David	Princeton	NJ	US	
Pollack, Brian P.	Highland Park	NJ	US	

APPL-NO: 10/ 239587

DATE FILED: March 13, 2003

PCT-DATA:
APPL-NO: PCT/US01/09087
DATE-FILED: Mar 22, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 435/193, 424/94.5 , 435/254.21

ABSTRACT:

The present invention relates to yeast protein Hs17p, which is a homologue of Janus kinase binding protein 1, JBP1. Hs17p is a newly characterized protein methyltransferase. The yeast protein Hs17p is a sequence and functional homologue of JBP1 indicating an intricate link between protein methylation and macroscopic changes in yeast morphology.

BACKGROUND OF THE INVENTION

[0001] This application claims priority from U.S. provisional patent application serial No. 60/191,614, filed Mar. 23, 2000.

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Detail Description Paragraph - DETX (31):

[0041] A number of methyltransferases have been identified in yeast: mRNA cap, rRNA, isoprenylcysteine and tRNA methyltransferases; two protein methyltransferases in S. cerevisiae: Rmt1p (also referred to as Hmt1p or Odp1p;) and Rmt2p. Rmt2p was discovered during a search for yeast proteins containing conserved AdoMet binding motifs, it methylates the .delta.-nitrogen atom of arginine residues, but its in vivo substrate proteins are not known. Rmt1p, on the other hand, is an **arginine methyltransferase** which methylates a number of yeast proteins such as Np13p and Hrp1p, which are hnRNPs and poly(A)+ RNA binding proteins. In vitro Rmt1p methylates mammalian hnRNP A1, cytochrome c, histones and myoglobin, but not myelin basic protein. Clearly, Hs17p exhibits different substrate specificity in vitro than Rmt1p. Hs17p methylates myelin basic protein whereas Rmt1p does not; Rmt1p methylates cytochrome c whereas Hs17p does not. These differences imply that Hs17p and Rmt1p play distinct cellular roles.

Detail Description Paragraph - DETX (35):

[0045] Although methylation of proteins such as the histones was recognized decades ago, a clear function for histone methylation has not been delineated. Recently, the **methyltransferase** CARM1 was reported to methylate histones H2A and H3 in vitro and enhance the **transcription of nuclear receptors, suggesting that it activates transcription** through histone methylation. The homologue of Hs17p, JBP1, interacts with all the Janus kinases (Jak1, Jak2, Jak3 and Tyk2), kinases required for signal transduction of interferons, cytokines and growth factors. As described above, Hs17p is intrinsically involved in at least two pathways: the Swe1p/Cdc28p morphogenesis checkpoint; and Ras signaling in the MAP kinase pathway. Furthermore, because Hs17p methylates histones, Hs17p is likely involved in chromatin remodeling and may contribute to the "histone code" that can control downstream events. Our data presented in this report provide evidence that there is an intricate link between protein methylation and yeast morphogenesis and other pathways such as Ras signaling and histone coding; and provide a biochemical basis for understanding the mechanism by which Hs17p modulates these many diverse actions.

PGPUB-DOCUMENT-NUMBER: 20030180808

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030180808 A1

TITLE: Drug signatures

PUBLICATION-DATE: September 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Natsoulis, Georges	Kensington	CA	US	

APPL-NO: 10/ 378002

DATE FILED: February 28, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60360728 20020228 US

US-CL-CURRENT: 435/7.1, 435/6 , 435/7.2 , 702/19

ABSTRACT:

Methods for deriving and using Group Signatures and Drug Signatures are provided, wherein Group Signatures comprise a plurality of genes, modulated expression of which is characteristic and specific of a group of related drug compounds, and wherein Drug Signatures comprise a plurality of genes, modulated expression of which is characteristic and specific for individual drug compounds.

[0001] This application claims the benefit of U.S. Provisional Application No. 60/360,728, filed Feb. 28, 2002.

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Detail Description Table CWU - DETL (4):

X53477 700304380 Rat p450Md mRNA for cytochrome P450 U15566 701560684 Mouse Tbx2 mRNA, complete cds D90038 700288719 Rat liver 70-kDa peroxisomal membrane protein (PMP70) mRNA AF202115 701463794 Rat GPI-anchored ceruloplasmin mRNA, complete cds S78221 700606373 nuclear protein TIF1 isoform (Mouse, mRNA, 4053 nt) #N/A 700138684 Mouse L-CaBP2 (Cabp2) mRNA, complete cds X53725 700329424 Rat MASH-1 mRNA expressed in neuronal precursor cells (mammalian achaete-scute homologue) U40397 700938882 Mouse serum amyloid A-4 protein (Saa4) gene, complete cds M23995 701521645 Rat aldehyde dehydrogenase mRNA, complete cds 0 700931483 Incyte EST D28566 701192728 Hamster mRNA for carboxylesterase precursor, complete cds M13590 700147294

Rat glutathione S-transferase Yb2 subunit mRNA, 3' end AAF09483 701644022 E2IG4 0 700515449 Incyte EST AB002558 700626043 Rat mRNA for glycerol 3-phosphate dehydrogenase, complete cds AJ302031 700503842 Rat liver regeneration-related protein 1 mRNA, complete cds D16479 700397284 Rat mRNA for mitochondrial long-chain 3-ketoacyl-CoA thiolase .beta.-subunit of mitochondrial trifunctional protein, complete cds AE000664 700503071 Mouse T-cell receptor .alpha. locus BAC clone MBAC519 from 14D1-D2, complete sequence AB010428 700146486 Rat mRNA for acyl-CoA hydrolase, complete cds AF117887 700245634 Mouse protein **arginine methyltransferase** (Carm1) mRNA, complete cds U43285 700368469 Mouse selenophosphate synthetase 2 mRNA, complete cds U42719 701438090 Rat C4 complement protein mRNA, partial cds AAA65642 700502628 apolipoprotein F S83247 700233325 DA11 = 15.2 kDa fatty acid binding protein/FABP/C-FAPB homolog (rats, Sprague-Dawley, sciatic nerve traumatized, dorsal root ganglia, mRNA Partial, 695 nt) AAA36986 700608519 glutathione S-transferase subunit pi M59189 701436793 Rat cholesterol 7.alpha.-hydroxylase gene, exon 6 0 701644979 Incyte EST AF116897 701193378 Mouse mahogany protein mRNA, complete cds M80427 700303313 Syrian golden hamster androgen-dependent expressed protein mRNA, complete cds M14201 700487123 Rat 11-Kd diazepam binding inhibitor (DBI), partial cds D88250 700372447 Rat mRNA for serine protease, complete cds #N/A 700063031 Rat VL30 element mRNA D37920 700491942 Rat mRNA for squalene epoxidase, complete cds U61266 700522707 Rat Rho-associated kinase .beta. mRNA, complete cds U02553 700187524 Rat protein tyrosine phosphatase mRNA, complete cds AF062389 700304757 Rat kidney-specific protein (KS) mRNA, complete cds D50559 700513027 Rat mRNA for RANP-1, complete cds K02422 701193624 Rat cytochrome P450d methylcholanthrene-inducible gene, complete cds X05684 701559151 Rat L-PK gene for L-type pyruvate kinase M11709 701345507 Rat L-type pyruvate kinase mRNA, complete cds M20131 700502447 Rat cytochrome P450IIE1 gene, complete cds X07266 700492544 Rat mRNA for gene 33 polypeptide V01222 701431070 Messenger RNA for rat preproalbumin J04632 700484528 Mouse glutathione S-transferase class .mu. (GST1-1) mRNA, complete cds J05430 701487679 Rat cholesterol 7.alpha.-hydroxylase (CYP7) mRNA, complete cds M77003 700331551 Mouse glycerol-3-phosphate acyltransferase mRNA, complete cds J03734 701194460 Rat Kupffer cell receptor mRNA, complete cds Z50051 700610324 R. norvegicus mRNA for Bovine C4BP .alpha.-chain protein 0 701437076 Incyte EST D90005 701430626 Rat endogenous retroviral sequence, 5' and 3' LTR BAB14526 701826510 oxidoreductase UCPA U38419 700609878 Rat dopa/tyrosine sulfotransferase mRNA, complete cds AF110477 701482962 Rat liver aldehyde oxidase female form (AOX1) mRNA, complete cds S74802 700178702 Rat beta-globin gene, exons 1-3 M34561 700146495 Rat 70 kd heat-shock-like protein mRNA, complete cds 0 701440048 Incyte EST X05341 700228787 Rat mRNA for 3-oxoacyl-CoA thiolase AF172276 701649184 Mouse aldehyde oxidase homolog-1 (Aoh1) mRNA, complete cds AF044574 701246587 Rat putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- AKL) mRNA, complete cds D90109 700527892 Rat mRNA for long-chain acyl-CoA synthetase (EC 6.2.1.3) #N/A 700137495 Rat pcRC201 mRNA for pre-pro-complement C3 X03430 700484501 Rat mRNA for L-type pyruvate kinase AF216873 700183232 Mouse acetyl-CoA synthetase mRNA, complete cds M58404 701562834 Rat thymosin .beta.-10 gene, complete cds M12516 700304405 Rat NADPH-cytochrome P450 reductase mRNA, complete cds 0 700501620 Incyte EST K03252 700481289 Rat prealbumin (transthyretin) mRNA, complete cds X52984 700609873 Rat mRNA for alpha(1)-inhibitor 3, variant I 0 700930555 Incyte EST 0 700328880 Incyte EST Z32548 701430793 Mouse TRGC78 DNA 414 bp 0 701518575 Incyte EST

BAA34502 700180621 KIAA0782 protein U49071 700304375 Rat complement component C9 precursor mRNA, partial cds AB012276 700528176 Mouse mRNA for ATFx, partial cds AB010632 700480022 Rat mRNA for carboxylesterase precursor, complete cds 0 700483266 Incyte EST J02861 701193056 Rat polymorphic, male-specific cytochrome P450g mRNA, complete cds AF200357 701258381 Mouse pantothenate kinase 1.beta. (panK1.beta.) mRNA, complete cds. D45252 701228305 Rat mRNA for 2,3-oxidosqualene: lanosterol cyclase, complete cds D17370 700307241 Rat mRNA for cystathionine gamma-lyase, complete cds M17083 700293050 Rat major alpha-globin mRNA, complete cds

PGPUB-DOCUMENT-NUMBER: 20030180739

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030180739 A1

TITLE: Reagents and methods for identifying gene targets for treating cancer

PUBLICATION-DATE: September 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Primiano, Thomas	Chicago	IL	US	
Chang, Bey-Dih	Lombard	IL	US	
Roninson, Igor B.	Wilmette	IL	US	

APPL-NO: 10/ 199820

DATE FILED: July 19, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60306730 20010720 US

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US02/06254	2002WO-PCT/US02/06254	February 28, 2002

US-CL-CURRENT: 435/6, 435/7.23 , 702/19

ABSTRACT:

The invention provides methods and reagents for identifying mammalian genes necessary for tumor cell growth as targets for developing drugs that inhibit expression of said genes and inhibit tumor cell growth thereby.

[0001] This application claims priority to U.S. Provisional Application Serial No.: 60/306,730, filed Jul. 20, 2001.

---------- KWIC ---------

Detail Description Table CWU - DETL (4):

4TABLE 3 Enriched Genes That Have Not Been Previously Implicated in Cell Proliferation # Sequences # Association with Gene Accession No. (s/as) clones Description cancer Transcription factors ATF4 NM_001675 5(as) 369 **Activating transcription** factor Induced in breast ca by heregulin HES6 XM_043579 1(s) 6 Transcription co-factor, differentiation inducer NR3C1 NM_000176 1(s) 5 Glucocorticoid receptor EDF1 NM_003792 1(s) 2 Transcription

factor, stimulates endothelial cell growth, represses endothelial cell differentiation MBD1 NM_015847 1(s), 1(as) 2 Methylated DNA binding protein, transcription inhibitor RNA transport HRPMT1L2 NM_001536 1(s) 5 Hnrp **arginine methyltransferase** HNRPF NM_004966 1(s) 5 Heterogeneous nuclear ribonucleoprotein F HNRPA2B1 NM_002137 1(s) 4 Heterogeneous nuclear ribonucleoprotein A2/B1 Signal transduction and cell adhesion ZIN NM_013403 1(as) 6 Calmodulin-binding WD repeat protein Arfaptin 1 NM_014447 1(as) 2 Similar to POR1 GTP-binding protein; may act in cellular membrane ruffling and formation of lamellipodia L1CAM NM_000425 8(s), 4(as) 20 Cell adhesion, neural ICAM2 NM_000873 2(s), 1(as) 8 Cell adhesion, intercellular Intracellular transport AP1B1/BAM22 NM_001127 2(s) 5 Clathrin-associated adaptor protein RAB2L NM_004761 1(s) 4 Small GTPase, intracellular transport Ras family KIFC1 XM_042626 1(as) 3 Intracellular trafficking Rab5B NM_002868 1(s), 1(as) 3 Small GTPase, vesicle transport Ras family Protein processing NIN283 NM_032268 1(s) 11 ubiquitin-mediated protein modification PSMB7 NM_002799 1(s) 4 Proteasome subunit .beta.7 SQSTM1 NM_003900 1(s) 2 Sequestosome 1; ubiquitin-mediated protein degradation RAD23A NM_005053 1(s) 2 Nucleotide excision repair, ubiquitin-mediated protein degradation Other VWF NM_000552 6(s), 5(as) 39 Blood clotting GSTP NM_000852 2(s) 8 Xenobiotic metabolism ENO1 NM_001428 2(s) 8 Glycolysis IF1 NM_016311 1(s) 4 Inhibitor of Fo/F1 mitochondrial ATPase MYL6 NM_021019 2(s) 2 Contractility FLJ13052 NM_023018 1(s) 2 NAD kinase (predicted) GBC-14 AL557138 1(s) 2 similar to tyrosine 3- monooxygenase/tryptopha- n 5- monooxygenase activation protein, zeta polypeptide KIAA1270 XM_044835 1(as) 9 Alanyl-tRNA synthetase homolog Unknown function GBC-1 NM_031221 2(s) 70 Contains helical repeat peptide FLJ10006 XM_041928 1(as) 2 GBC-3 AA443027 1(s) 12 HC 3q29 GBC-11 1(s) 4 HC 14 GBC-12 1(s) 3 HC 1 GBC-13 1(s) 2 GBC-15 BE079876 1(s) 2 GBC-16 1(s) 2 GBC-17 1(s) 2 GBC-18 1(s) 2

PGPUB-DOCUMENT-NUMBER: 20030180713

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030180713 A1

TITLE: Cells for drug discovery

PUBLICATION-DATE: September 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Case, Casey	San Mateo	CA	US	

APPL-NO: 10/ 412109

DATE FILED: April 10, 2003

RELATED-US-APPL-DATA:

child 10412109 A1 20030410

parent division-of 09779233 20010208 US PENDING

non-provisional-of-provisional 60181117 20000208 US

US-CL-CURRENT: 435/4, 435/6 , 435/7.2

ABSTRACT:

Disclosed herein are compositions and method useful in screening a compound for its interaction and/or effect with a molecular target and/or cellular process.

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application is related to provisional patent application serial No. 60/181,117, filed Feb. 8, 2000, from which priority is claimed under 35 USC .sctn.119(e)(1) and which is incorporated herein by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (61):

[0084] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos and/or erb family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their

modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20030176678

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030176678 A1

TITLE: Novel IFN receptor 1 binding proteins, DNA encoding them, and methods of modulating cellular response to interferons

PUBLICATION-DATE: September 18, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Revel, Michel	Rehovot		IL	
Abramovitch, Carolina	Yavne		IL	
Chebath, Judith E.	Rehovot		IL	

APPL-NO: 10/ 309280

DATE FILED: December 4, 2002

RELATED-US-APPL-DATA:

child 10309280 A1 20021204

parent continuation-of 09341640 19991008 US ABANDONED

child 09341640 19991008 US

parent a-371-of-international PCT/US98/00671 19980115 WO PENDING

non-provisional-of-provisional 60035636 19970115 US

US-CL-CURRENT: 536/23.1

ABSTRACT:

Novel proteins IR1B1 and IR1B4 have been isolated which bind to the type I IFN receptor IFNAR1 and function in the cellular response to IFNs. DNA encoding such proteins in either the sense or anti-sense orientation can be administered to either enhance or inhibit the cellular response to IFNs. Antibodies to the proteins can be used for isolation of the new protein or for immunodetection thereof.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a continuation of U.S. application Ser. No. 09/341,650, filed Oct. 8, 1999, which is the national stage under 35 U.S.C. 371 of PCT/US98/00671, filed Jan. 15, 1998, which international application claims the benefit under 35 U.S.C. .sctn.119(e) of U.S. provisional

application No. 60/035,636, filed Jan. 15, 1997, now abandoned.

---------- KWIC ---------

Brief Description of Drawings Paragraph - DRTX (12):

[0023] FIG. 11 shows an assay of protein-**arginine methyltransferase** activity in U266S cells. In lane 1, the protein-**arginine methyltransferase** activity of human U266S cells was measured by methylation of peptide R1, having the sequence of SEQ ID NO: 11. In lane 2 an anti-sense oligonucleotide of SEQ ID NO: 12, complementary to the sequence of nucleotides 12-33 around the initiation codon of IR1B4 cDNA, was added. In lane 3 the corresponding sense oligonucleotide was added. It is seen that the anti-sense oligonucleotide substantially inhibits the protein-**arginine methyltransferase** activity while the control sense oligonucleotide has little effect.

Detail Description Paragraph - DETX (5):

[0028] While IR1B4, like IR1B1, was found to be a novel protein as determined by computer searches of sequence databases, it was also found that IR1B4 has sequence homology to enzymes which utilize S-adenosyl methionine for methylating arginine residues in proteins and are designated as protein **arginine methyltransferases** (PRMT1; Kagan and Clarke, 1994; Lin et al, 1996). IR1B4 was found to bind directly to the IC-domain of IFNAR1 in vitro, and the constitutive association of PRMT activity with the IFNAR chain of the IFN-.alpha., .beta. receptor isolated from human cells was demonstrated by methylation of histones. When anti-sense oligodeoxynucleotides from the IR1B4 cDNA was added to human cell cultures, depletion of PRMT activity in the cell culture was observed. Human myeloma cells that were treated in this manner showed a much reduced response to IFN as measured by growth-inhibition. Therefore, IR1B4/PRMT is involved in the pathway by which the IFN receptor causes growth-inhibition in tumor cells and is also involved in other functions of the IFN receptor. Known substrates of PRMT include a number of RNA and DNA binding proteins, and in particular heterologous nuclear ribonucleoproteins (hnRNPs). The hnRNPs are involved in mRNA transport from the nucleus to the cytoplasm, alternative splicing of pre-mRNA, and post-transcriptional controls (Liu and Dreyfuss, 1995). Accordingly, the novel human IR1B4/PRMT cDNA and protein, which were discovered by its association with the IFN receptor, can be used to modify the response of human or animal cells to IFN.

Detail Description Paragraph - DETX (15):

[0038] The anti-sense sequence need not hybridize to the entire length of the IR1B1 or IR1B4 mRNA. Instead, it may hybridize to selected regions, such as the 5'-untranslated non-coding sequence, the coding sequence, or the 3'-untranslated sequence of the "sense" mRNA. Preferably, the anti-sense sequence hybridizes to the 5'-coding sequence and/or 5'-non-coding region, such as at cap and initiation codon sites, since it has been observed it has been observed with many examples of anti-sense oligonucleotides that targeting the initiation codon is more effective, whereas targeting internal sequences within the coding region is not as effective (Wickstrom, 1991). The effectiveness of an anti-sense sequence in preventing translation of IR1B4 sense mRNA can easily

be tested in an assay for protein-**arginine methyltransferase** activity in U266S cells as described in Example 7. In view of the size of the mammalian genome, the anti-sense IR1B1 or IR1B4 sequence is preferably at least 17, more preferably at least 30 base pairs in length. However, shorter sequences may still be useful, i.e., they either fortuitously do not hybridize to other mammalian sequences, or such "cross-hybridization" does not interfere with the metabolism of the cell in a manner and to a degree which prevents the accomplishment of the objects of this invention.

Detail Description Paragraph - DETX (57):

[0075] The nucleotide sequence of the IR1B4 cDNA has an open reading frame encoding a 361 amino-acid long protein (FIG. 7). This human cDNA recognized a 1.5 kb constitutively expressed poly-A.sup.+ mRNA in various human cells including U266 myeloma cells. An online search of the protein databases was performed using the BlastP algorithm (Altschul et al, 1990) as well as the Bioaccelerator Alignment (Henikoff and Henikoff, 1992), and it was found that IR1B4 is a unique member of the protein-**arginine methyltransferase** family. The rat PRMT1 cDNA described by Lin et al (1996, Genbank sequence I.D. 1390024; Accession U60882) is only 81.4% homologous when analyzed by the ALIGN computer program. At the amino acid level (FIG. 8), the human IR1B4/PRMT differs clearly in its amino terminus from PRMT1, with the first 19 amino acids being completely different. N-terminal sequencing of IR1B4 alone would not have provided any indication that IR1B4 is homologous to PRMT1. Another human protein which has been described, HCP-1 (Nikawa et al, 1996; Genbank accession D66904) was also found to have homology to IR1B4. However, HCP-1 has a different amino acid sequence from residues 147-175 (FIG. 9). HCP-1 was originally identified based on its ability to complement the irel5 mutation in yeast and its enzymatic function was not previously identified (Nikawa et al, 1996). Therefore, IR1B4 is a novel human protein.

Detail Description Paragraph - DETX (63):

[0079] An antisense oligodeoxynucleotide phosphorothioate (Stein et al, 1989) complementary to the sequence of nucleotides 12-33 around the initiation codon of IR1B4 cDNA (AS-1, anti-sense sequence 5'GGCTACAAAATTCTCCATGATG-3'; SEQ ID NO: 12) was synthesized chemically. The oligonucleotides were added to U266S cells seeded in 96-well microplates (8000 cells/well/0.2 ml RPMI, 10% FCS) at a final concentration of 10 .mu.M on day 0 and re-added at 5 .mu.M on day 2. IFN-.beta. was added at 64 or 125 IU/ml on day 0. After 3 days of culture, 20 .mu.l of Alamar Blue, a colorimetric cell density indicator based on oxido-reduction (BioSource, Camarillo, Calif.), was added to each well and incubation continued for 6-7 h. Color was measured in a microplate ELISA reader (test filter 530 nm, reference filter 630 nm) with multiple reading of duplicate wells. Correlation of the growth curves by live cell number and by OD was verified. To measure methyltransferase, cells from pooled wells were lysed by freeze-thawing in 25 .mu.l/well of 25 mM Tris-HCl, pH 7.4, 1 mM EDTA, 1 mM EGTA, 40 .mu.g/ml leupeptin and aprotinin, 20 .mu.g/ml pepstatin, 1 UM phenylmethylsulfonyl fluoride (PMSF). Reactions were in 50 .mu.l with 25 .mu.l of cell extracts, 100 .mu.M peptide R1 (Najbauer et al, 1993; obtained from Genosys, Cambridge, UK), 3 .mu.Ci of [.sup.3H] (methyl)S-adenosylmethionine (Amersham, 73 Ci/mmol) for 30 min at 30.degree. C. After electrophoresis in SDS-polyacrylamide (16%) gel, fixation in 50% methanol, 10% acetic acid and

treatment by Amplify (Amersham), autoradiography was carried out for 8 days. This AS-1 anti-sense DNA was able to strongly reduce the protein-**arginine methyltransferase** activity in U266S cells as measured by incorporation of tritiated-methyl groups to the R1 peptide substrate (FIG. 11), and was used to investigate the role that this enzyme may play in IFN action. The growth-inhibitory activity of IFN was chosen because it can be most directly quantified on cells and because an interaction of rat PRMT1 with growth-related gene products has been observed (Lin et al, 1996). Addition of the antisense-1 oligonucleotide AS-1, which is complementary to the sequence around the initiation codon of IR1B4/PRMT cDNA, reduced the growth inhibitory effect of IFN-.beta. on human myeloma U266S cells (FIG. 12). This means that, in the presence of anti-sense AS-1, the IFN-treated cells exhibited a higher growth (excluding any toxic effect of phosphorothioates). The growth in the absence of IFN was not significantly affected. The sense oligonucleotide S-3 corresponding to the same cDNA region had only a small effect (S-3, FIG. 12) as compared to antisense-1. Sense S-3 also had only a slight inhibitory effect on the level of enzyme activity (FIG. 11). Another anti-sense phosphorothioate oligonucleotide AS-2 (SEQ ID NO: 13), directed to the middle of the cDNA and complementary to nucleotides 572-592 of SEQ ID NO: 7, had almost no effect (FIG. 12). The up to 5 fold reduction in the growth inhibitory effect of IFN-.beta. on myeloma cells, which were rendered partially deficient in PRMT activity by antisense-1 oligonucleotide demonstrates that the association of the IR1B4/PRMT enzyme with the IC domain of the IFNAR1 receptor is functionally significant for IFN action on cells.

Detail Description Paragraph - DETX (95):

[0110] Lin et al, "The mammalian immediate-early TIS21 protein and the leukemia-associated BTG1 protein interact with a Protein-**arginine Methyltransferase**", J Biol Chem 271:15034-15044 (1996)

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PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030175923 A1

TITLE: Human transferase proteins

PUBLICATION-DATE: September 18, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 427631

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non-provisional-of-provisional 60155248 19981104 US

non-provisional-of-provisional 60133642 19990511 US

US-CL-CURRENT: 435/193, 435/320.1 , 435/325 , 435/6 , 435/69.1 , 536/23.2 , 800/8

ABSTRACT:

The invention provides human human transferase proteins (TRNSFS) and polynucleotides which identify and encode TRNSFS. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The

invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of TRNSFS.

[0001] This application is a divisional application of U.S. application Ser. No. 09/786,240, filed Mar. 12, 2002, now U.S. Pat. No. 6,558,935, issued May 6, 2003, which is the National Stage of International Application No. PCT/US99/20989, filed on Sep. 9, 1999, which claims the benefit under 35 U.S.C. .sctn. 119(e) of U.S. Provisional Application Serial No. 60/172,220, filed Sep. 10, 1998, and U.S. Provisional Application Serial No. 60/155,248, filed Nov. 4, 1998, and U.S. Provisional Application Serial No. 60/133,642, filed on May, 11, 1999, the contents all of which are hereby incorporated herein by reference.

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Summary of Invention Paragraph - BSTX (13):

[0012] The enzyme glycine N**-methyltransferase** catalyzes the transfer of the methyl group from S-adenosylmethionine to glycine to form S-adenosylhomocyteine and sarcosine. Glycine N**-methyltransferase** is a tetramer of identical subunits, has a nucloetide binding region, and is localized in the liver. Amino acid sequence homology is found between glycine N-methlytransferases from rat, rabbit, pig, and human livers. Glycine N**-methyltransferase** can exist as a dimer which binds polycyclic aromatic hydrocarbons (PAHs) and acts as a **transcriptional activator** (Ogawa, H. et al. (1998) Int. J. Biochem. Cell Biol. 30:13-26; Bhat, R. and Bresnick, E. (1997) J. Biol. Chem. 272:21221-21226).

PGPUB-DOCUMENT-NUMBER: 20030175790

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DOCUMENT-IDENTIFIER: US 20030175790 A1

TITLE: Cells for drug discovery

PUBLICATION-DATE: September 18, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 412105

DATE FILED: April 10, 2003

RELATED-US-APPL-DATA:

child 10412105 A1 20030410

parent division-of 09779233 20010208 US PENDING

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US-CL-CURRENT: 435/6, 435/7.2

ABSTRACT:

Disclosed herein are compositions and method useful in screening a compound for its interaction and/or effect with a molecular target and/or cellular process.

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application is related to provisional patent application serial no. 60/181,117, filed Feb. 8, 2000, from which priority is claimed under 35 USC .sctn.119(e)(1) and which is incorporated herein by reference in its entirety.

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Detail Description Paragraph - DETX (61):

[0084] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos and/or erb family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their

modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

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DOCUMENT-IDENTIFIER: US 20030166562 A1

TITLE: Treatment for asthma or allergies

PUBLICATION-DATE: September 4, 2003

INVENTOR-INFORMATION:

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Zimmermann, Nives	Cincinnati	OH	US	

APPL-NO: 10/ 377998

DATE FILED: February 28, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60361606 20020301 US

US-CL-CURRENT: 514/12, 435/6 , 435/7.1

ABSTRACT:

Several genes are upregulated in the lung of asthma or allergy sufferers. Many of the genes up-regulated in asthma are involved in arginine metabolism in the lung. Moreover, a set of 291 signature genes was found that can be used to indicate a patient's predilection for developing asthma or the patient's degree of suffering. Also, a set of 59 signature genes were found that indicate a patient's predilection for developing allergies. Many of the up-regulated genes relating to asthma were from the arginine metabolic pathway. Other genes, such as ADAM8, SPRR2A and SPRR2B were also strongly up-regulated in asthma. Treatment of asthma may be accomplished by administering compositions which decrease the levels of Arginase I, Arginase II, CAT2, or other arginase pathway members in the lung. Additionally, detection of altered levels of these proteins or the mRNA encoding them may be useful to diagnose the presence of asthma in a patient.

RELATED APPLICATIONS

[0001] This application claims priority from U.S. Provisional application 60/361,606 filed on Mar. 1, 2002.

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Detail Description Table CWU - DETL (2):

99979_at 3.879566 4.449123 NM_009994 cytochrome P450, 1b1, benz[a]anthracene inducible 102755_at 3.8250763 42.851036 NM_010584 intelectin 99876_at 3.7478104 2.71695 AJ131777 src-like adaptor protein 100771_at 3.7049873 52.361767 Y17159 lymphocyte antigen 57 102025_at 3.746413 11.825412 NM_018866 SCYB13 (BLC/BCA-1) 101521_at 3.7192738 3.4149444 BC004702 baculoviral IAP repeat-containing 5 98562_at 3.5959404 3.0973809 NM_007572 complement component 1, q subcomponent, alpha polypeptide 100116_at 3.8081882 2.2723222 NM_026515 EST 103210_at 3.5521066 3.5796819 NM_007781 colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage) 97444_at 3.5403333 3.7394972 NM_023065 interferon gamma inducible protein 30 103040_at 3.5184398 5.563819 NM_009856 CD83 antigen 92832_at 3.5796704 2.58255 NM_009896 cytokine inducible SH2-containing protein 1 101468_at 3.499593 2.9337993 X12905 properdin factor, complement 101656_f_at 3.572765 5.152894 U68543 immunoglobulin kappa chain 160406_at 3.5679104 6.6120887 AJ006033 ctsk 161511_f_at 3.6552558 2.4223258 AK019325 EST 100479_at 3.5037563 5.1488533 NM_007872 DNA **methyltransferase** 3A 96784_at 3.5443184 7.2892175 BE573736 EST 98473_at 3.414378 4.315487 NM_009705 arginase II 103690_at 3.4046066 2.7740142 AW125574 EST 97411_at 3.432237 5.097896 NM_007900 ect2 oncogene 102990_at 3.3784416 3.176364 AK019448 procollagen, type III, alpha 1 101913_at 3.3619032 2.298871 NM_010423 hairy/enhancer-of-split related with YRPW motif 1 96511_s_at 3.349278 2.489442 NM_011691 vav oncogene 96515_at 3.3318715 5.013796 U70430 estrogen receptor beta 99509_s_at 3.304514 2.4309058 NM_010589 Janus kinase 3 102658_at 3.29768 2.4413974 NM_010555 interleukin 1 receptor, type II 99405_at 3.4179718 2.6559134 Z95479 immunoglobulin kappa chain 102001_at 3.2696967 4.6717634 NM_009104 ribonucleotide reductase M2 100772_g_at 3.2473373 3.9850318 Y17159 lymphocyte antigen 57 100156_at 3.2375228 5.1784253 NM_008566 mini chromosome maintenance deficient 5 102884_at 3.2394269 5.047297 NM_010566 inositol polyphosphate-5-phosphatase, 145 kDa 98772_at 3.2060094 9.574579 NM_009141 SCYB5 (LIX) 98859_at 3.1933463 3.7756183 M99054 glucose dependent insulinotropic polypeptide 93465_at 3.1908364 2.0911632 AK020278 EST 102697_at 3.2435853 50750 NM_019640 phosphotidylinositol transfer protein, beta 104548_at 3.1858604 2.3911338 NM_009434 tumor-suppressing subchromosomal transferable fragment 3 160446_at 3.0992258 2.0170536 U46068 von Ebner minor salivary gland protein mRNA 92918_at 3.2433689 3.870666 U66079 coagulation factor VII 99926_at 3.0930579 2.6117299 AB001489 EST 98034_at 3.0988965 2.399438 NM_010387 histocompatibility 2, class II, locus Mb1 103441_at 3.1662524 2.6342456 NM_007788 casein kinase II, alpha 1 related sequence 4 101868_i_at 3.0873947 3.2774441 NM_010388 histocompatibility 2, class II, locus Mb2 104065_at 3.104958 2.903548 AB042828 EDEM, similar to alpha-mannosidase 103418_at 3.0449538 4.5369325 BC003335 EST 103201_at 3.1155026 2.5040376 NM_009445 Ttk protein kinase 102892_at 2.965567 2.3691757 U31908 potassium voltage-gated channel, shaker-related subfamily, beta member 2 101020_at 3.0216243 4.072408 NM_009982 cathepsin C 102372_at 2.962975 4.9571853 BC006026 immunoglobulin joining chain 96295_at 2.980223 4.0674667 BC004827 DNA segment, Chr 8, ERATO Doi 814, expressed 103089_at 2.977104 2.9797423 X53526 CD48 antigen 160663_at 3.0093396 3.73139 BC011308 EST 160119_at 2.9357014 2.8572135 NM_007961 TEL oncogene 104547_at 3.0306945 2.5664012 J00388 dihydrofolate reductase gene 162198_f_at 2.930065 3.8110802 NM_009139 SCYA6 (C10, MRP-1) 98948_at 2.913645 2.3195322 BE914613 EST 92472_f_at 2.915114 2.61941 NM_011408 schlafen 2 92232_at 2.943417 3.4743614 NM_007707 cytokine inducible SH2-containing protein 3 101878_at 2.8530445 4.578556 NM_007654 CD72 antigen 94294_at

2.7738435 2.6131907 NM_007630 cyclin B2 AFFX- 2.8628469 39776.668 NM_011638 transferring receptor TransRecMur/ X57349_M_at 102809_s_at 2.7613506 2.1943572 BC011474 lymphocyte protein tyrosine kinase 99973_s_at 2.749837 5.1267667 NM_019664 potassium inwardly-rectifying channel, subfamily J, member 15 103205_at 2.698056 3.892967 NM_016921 T-cell, immune regulator 1 97421_at 2.7415438 2.267686 NM_008017 fibroblast growth factor inducible 16 95148_at 2.6961179 2.801927 NM_016895 adenylate kinase 2 95032_at 2.7158015 6.0467033 BC005475 DNA segment, Chr 7, ERATO Doi 348, expressed 95532_at 2.7031207 2.6633081 BG070246 EST 98035_g_at 2.6737032 2.1324506 NM_010387 histocompatibility 2, class II, locus Mb1 161103_at 2.6972256 7.9766407 BG064768 EST 103662_at 2.6623814 2.36007 NM_008677 neutrophil cytosolic factor 4 104464_s_at 2.6995149 2.8936243 BC011472 EST 160298_at 2.701887 2.6409597 AK011256 EST 162206_f_at 2.6395187 2.7735467 NM_007707 cytokine inducible SH2-containing protein 3 102310_at 2.622947 2.9848456 NM_009137 SCYA22 (ABCD-1) 98433_at 2.5899887 2.410541 BC002031 BH3 interacting domain death agonist 99974_at 2.6164083 6.7606096 NM_019664 potassium inwardly-rectifying channel, subfamily J, member 15 104099_at 2.6075976 2.9022658 NM_009402 peptidoglycan recognition protein 104147_at 2.568291 2.4725318 NM_053179 sialic acid synthase 101506_at 2.5859814 2.4086373 NM_021336 U2 small nuclear ribonucleoprotein polypeptide A' 103203_f_at 2.611314 4.093791 W29450 EST 93112_at 2.5585814 3.6827056 NM_008564 mini chromosome maintenance deficient 2 104097_at 2.586194 4.50625 U89795 budding uninhibited by benzimidazoles 1 homolog 99669_at 2.5426898 2.2998266 NM_008495 lectin, galactose binding, soluble 1 99149_at 2.6465125 4.2806926 NM_025863 EST 102326_at 2.535973 4.4882274 NM_010877 neutrophil cytosolic factor 2 102293_at 2.5311453 2.1284976 NM_009578 zinc finger protein, subfamily 1A, 1 (Ikaros) 92833_at 2.515559 5.7817793 NM_010401 histidine ammonia lyase 92540_f_at 2.5182536 2.2194166 Z67748 spermidine synthase gene 92633_at 2.4970362 4.8684945 NM_022325 cathepsin Z 94521_at 2.5898051 2.126383 NM_009878 cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) 102748_at 2.5555553 3.159657 NM_007976 coagulation factor V 98026_g_at 2.4942427 2.6773672 NM_010161 ecotropic viral integration site 2 104155_f_at 2.4959242 3.0125077 U19118 **activating transcription** factor 3 104606_at 2.476346 2.9692168 NM_013706 CD52 antigen 95423_at 2.4727428 2.26199 NM_009787 calcium binding protein, intestinal 102914_s_at 2.4644232 2.763536 U23778 hematopoietic-specific early-response A1-b 100322_at 2.506151 3.7979157 U68543 immunoglobulin kappa chain 101561_at 2.5639465 3.3606117 K02236 metallothionien II 94208_at 2.4507363 2.1223657 AK005989 EST 92978_s_at 2.5112484 57173.336 NM_011111 serine (or cysteine) proteinase inhibitor,. clade B (ovalbumin), member 2 98968_at 2.4667523 3.6377416 NM_010864 myosin Va 93869_s_at 2.409471 2.9823458 U23781 hematopoietic-specific early-response A1-d 100955_at 2.4169822 2.8062625 NM_026024 EST 94939_at 2.3913658 2.5653691 NM_007651 CD53 antigen 94831_at 2.3831258 2.396902

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INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/199, 424/94.6 , 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

The purification of native RB (retinoblastoma) as a complex, including P107, P130, and a 600 kDa subunit, termed MTAF600 (microtubule associated factor 600) is described. MTAF600 binds to RB regardless of the phosphorylation status of RB, and binds to RB without disrupting the interaction between RB and E2F. It is further shown that E2F and DP proteins co-purified with MTAF600 and RB, such that hypophosphorylated RB may gain access to E2F as a complex with MTAF600. In addition, MTAF600 binds to microtubules and plays a role in active repression of E2F-responsive genes, cell cycle arrest, and genomic stability. The sequence of MTAF600 is described herein, along with its binding properties to proteins such as RB and microtubules, and its sequence homology. Further, methods and reagents for assaying the presence of MTAF600 or mutants thereof, pharmaceutical formulations, and methods for treating disease are also described.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application gains priority from provisional application serial No. 60/278,245 and provisional application 60/278,244 both filed on Mar. 23, 2001 and incorporated herein by reference.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (3):

[0003] The failure of normal function of the retinoblastoma tumor suppressor gene (RB) has been implicated as a contributing factor in a number of tumor types, including retinoblastomas and osteosarcomas, as well as lung, breast, and bladder carcinomas. (For reviews, see Goodrich et al., Biochim. Biophys. Acta., Vol. 1155, pp. 43-61, 1993; Zacksenhaus et al., Adv. Cancer. Res., Vol. 61, pp. 115-141, 1993; Sellers et al., J. Clin. Oncol., Vol. 15, pp. 3301-3312, 1997; Lohmann, D. R., Hum. Mutat., Vol. 14, pp. 283-288, 1999). A major role of RB is repression of the E2F family of DNA-binding **transcriptional activators,** which regulate the cell cycle through various genes required for S-phase entry. In resting cells, RB exists in the hypophosphorylated form that binds directly to E2F. (Reviewed in Weinberg, R. A., Cell, Vol. 81, pp. 323-330, 1995; Dyson, N., Genes Dev., Vol. 12, pp. 2245-2262, 1998). Importantly, mutations in E2F-recognition sequences, at least in some promoters, lead to derepression in G0/G1 cells, rather than repression in S-phase. (Neuman et al., Mol. Cell. Biol., Vol. 14, pp. 6607-6615, 1994). Although RB binds to the promoters only through E2F, RB is capable of repressing not only E2F, but also various activators that bind to E2F-responsive promoters. It has been proposed that chromatin modifiers, including histone deacetylases, (Brehm et al, Nature, Vol. 391, pp. 597-601, 1998), ATP-dependent chromatin remodeling factors (Zhang et al., Cell, Vol. 101, pp. 79, 2000), and DNA **methyltransferases** (Fuks et al., Nat. Genet., Vol. 24, pp. 88-91, 2000; Robertson et al., Nat. Genet., Vol. 25, pp. 338-3342, 2000) are involved in the mechanisms of this active repression. (Harbour et al., Curr. Opin. Cell Biol., Vol. 12, pp. 685-689, 2000).

Detail Description Paragraph - DETX (33):

[0092] First, histone acetylases (HDAC1, 2 and 3) have been shown to interact directly with RB. (Brehm et al., Nature, Vol. 391, pp. 597-601, 1998; Ferreira et al., Proc. Natl. Acad. Sci. U.S.A., Vol. 95, pp. 10493-10498, 1998; Luo et al., Cell, Vol. 92, pp. 463-473, 1998; Magnaghi-Jaulin et al., Nature, Vol. 391, pp. 601-605, 1998). Acetylation of core histone tails plays an important role in **transcriptional activation** in chromatin contexts. Recruitment of histone deacetylases to promoters via E2F and RB could allow them to alter acetylation status and maintain chromatin in a hypoacetylated state. Moreover, RB and DNA **methyltransferase** appear to be functionally related. (Fuks et al., Nat. Genet., Vol. 24, pp. 88-91, 2000; Robertson et al., Nat. Genet., Vol. 25, pp. 338-3342, 2000). Although the molecular mechanisms are unclear, methylation of the CpG island is associated with transcriptional silencing and the formation of high-ordered chromatin structures enriched in hypoacetylated histones. The finding that the DNA **methyltransferase** DNMT1 copurifies with HDAC1, RB, and E2F (Robertson et al., Nat. Genet., Vol. 25, pp. 338-3342, 2000) suggests that targeted methylation as well as deacetylation in E2F-responsive promoters may contribute to active repression.

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TITLE: Regulation of endogenous gene expression in cells using zinc finger proteins

PUBLICATION-DATE: September 4, 2003

INVENTOR-INFORMATION:

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DATE FILED: September 16, 2002

RELATED-US-APPL-DATA:

child 10245415 A1 20020916

parent continuation-in-part-of 09229007 19990112 US GRANTED

parent-patent 6453242 US

child 10245415 A1 20020916

parent continuation-in-part-of 09229037 19990112 US GRANTED

parent-patent 6534261 US

child 10245415 A1 20020916

parent continuation-in-part-of 09731558 20001206 US GRANTED

parent-patent 6503717 US

child 09731558 20001206 US

parent continuation-in-part-of 09456100 19991206 US ABANDONED

US-CL-CURRENT: 435/69.1, 435/320.1 , 435/325 , 435/366 , 435/456 , 702/19

ABSTRACT:

The present invention provides methods for modulating expression of endogenous cellular genes using engineered zinc finger proteins.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of copending U.S. patent application Ser. No. 09/229,007, filed Jan. 12, 1999, Ser. No. 09/229,037, filed Jan. 12, 1999, and Ser. No. 09/731,558, filed Dec. 6, 2000 (Ser. No. 09/731,558 being itself a continuation-in-part of U.S. patent application Ser. No. 09/456,100, filed Dec. 6, 1999, now abandoned). The present application claims priority under 35 U.S.C. .sctn. 120 to all of the aforementioned applications, the disclosures of which are hereby incorporated by reference in their entireties.

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Detail Description Paragraph - DETX (33):

[0073] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (117):

[0157] Common regulatory domains for addition to the ZFP include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, re1, ets, bc1, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20030165903

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030165903 A1

TITLE: Chimeric histone acetyltransferase polypeptides

PUBLICATION-DATE: September 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Dang, Van-Dinh	Oak Park	CA	US	
Okamuro, Jack	Oak Park	CA	US	

APPL-NO: 10/ 177478

DATE FILED: June 21, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60300135 20010622 US

US-CL-CURRENT: 435/6, 435/196 , 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

Chimeric polypeptides are disclosed that comprise a first polypeptide segment having histone acetyltransferase enzymatic activity and a second polypeptide segment that is similar to a subunit of a chromatin-associated histone deacetyltransferase protein complex. Also disclosed are nucleic acids encoding such chimeric polypeptides and eukaryotic organisms expressing such chimeric polypeptides.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Application Serial No. 60/300,135, filed on Jun. 22, 2001.

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Summary of Invention Paragraph - BSTX (16):

[0014] The invention also features eukaryotic organisms that contain: 1) a first nucleic acid construct having a first promoter and a **transcription activator** element operably linked to a coding sequence that encodes a chimeric polypeptide, and 2) a second nucleic acid construct having a second promoter conferring cell type-specific transcription operably linked to a coding sequence for a polypeptide that binds the **transcription activator** element. The encoded chimeric polypeptide has: 1) a first polypeptide segment that exhibits

histone acetyltransferase activity, and 2) a second polypeptide segment that has 40% or greater sequence identity to a subunit of a histone deacetylase chromatin-associated protein complex. The first and second polypeptide segments of an encoded chimeric polypeptide are arranged such that a terminus of the second polypeptide segment is covalently linked to a terminus of the first polypeptide segment. In some embodiments, the organism is an animal. In other embodiments the organism is a plant (e.g., a monocot such as corn and rice, or a dicot such as soybean and rape). In some embodiments, the plant contains a mutation or agent that alters (i.e., increases or decreases) the DNA methylation state in the plant relative to a corresponding plant that lacks said agent or mutation. In some embodiments, the mutation is in a C5 DNA **methyltransferase** (a.k.a. cytosine C5 DNA **methyltransferase**) gene. In some embodiments, the agent is an antisense nucleic acid. In some embodiments, the agent affects expression of a C5 DNA **methyltransferase** gene.

PGPUB-DOCUMENT-NUMBER: 20030154032

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030154032 A1

TITLE: Methods and compositions for diagnosing and treating rheumatoid arthritis

PUBLICATION-DATE: August 14, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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Feldman, Jeffrey L.	Arlington	MA	US	
Shields, Kathleen M.	Harvard	MA	US	
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APPL-NO: 10/ 023451

DATE FILED: December 17, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60255861 20001215 US

US-CL-CURRENT: 702/20

ABSTRACT:

The invention provides methods and compositions for diagnostic assays for detecting R.A. and therapeutic methods and compositions for treating R.A. The invention also provides methods for designing, identifying, and optimizing therapeutics for R.A. Diagnostic compositions of the invention include compositions comprising detection agents for detecting one or more genes that have been shown to be up- or down-regulated in cells of R.A. relative to normal counterpart cells. Exemplary detection agents include nucleic acid probes, which can be in solution or attached to a solid surface, e.g., in the form of a microarray. The invention also provides computer-readable media comprising values of levels of expression of one or more genes that are up- or down-regulated in R.A.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 60/255,861, filed Dec. 15, 2000, the contents of which are specifically incorporated by reference herein.

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Detail Description Table CWU - DETL (53):

15.15 1.31 1.31 CBFA3 1p36 core-binding factor, core-binding factor, runt domain, alpha runt domain, alpha subunit 3 subunit 3 PSMCP31 D38047_at D38047 PASS 9 31.22 PASS 13 9 23.92 1.31 1.31 PSMD8 proteasome (prosome, proteasome (prosome, macropain) 26S subunit, macropain) 26S subunit, non-ATPase, 8 non-ATPase, 8 PSM42 D78275_at D78275 PASS 8 9.25 PASS 10 8 7.10 1.30 1.30 PSMC6 12q15 proteasome (prosome, proteasome (prosome, macropain) 26S subunit, macropain) 26S subunit, ATPase, 6 ATPase, 6 P76 U81006_at U81006 PASS 7 9.00 PASS 11 7 6.91 1.30 1.30 P76 76 kDa membrane protein 76 kDa membrane protein K54_MOV10 D29677_at D29677 PASS 7 8.29 PASS 11 7 6.36 1.30 1.30 KIAA0054 SKIP U51432_at U51432 PASS 6 13.00 PASS 10 6 10.00 1.30 1.30 nuclear protein Skip similar to the Drosophila puff specific protein Bx42 K276 D87445_at D87445 PASS 6 6.50 PASS 9 6 5.00 1.30 1.30 KIAA0256 KIAA0256 gene product LGALS8 L78132_at L78132 PASS 6 6.17 PASS 8 6 4.75 1.30 1.30 peta-1 prostate carcinoma tumor antigen POLR2 U37689_at U37689 PASS 5 9.80 PASS 9 5 7.56 1.30 1.30 hsRPB8 RNA polymerase II subunit CASP10 U60519_at U60519 PASS 6 6.67 PASS 7 6 5.14 1.30 1.30 CASP10 2q33-q34 caspase 10, apoptosis- caspase 10, apoptosis- related cysteine protease related cysteine protease L14778_s_at L14778.sub.'s_at L14778 PASS 9 9.78 PASS 11 9 7.55 1.30 1.30 PPP3CA 4q21-q24 calmodulin-dependent protein phosphatase 3 phosphatase catalytic (formerly 2B), catalytic subunit subunit, alpha isoform (calcineurin A alpha) RAB_rna1 L42025_rna1 L42025 PASS 6 6.33 PASS 9 6 4.89 1.30 1.30 HRB 2q36 HIV-1 Rev binding protein HIV-1 Rev binding protein GAPDHM AFFX-HUM AFFX-HUM PASS 9 162.00 PASS 13 9 125.31 1.29 1.29 E_121711DM U92014_at U92014 PASS 6 6.83 PASS 7 6 5.29 1.29 1.29 HRMT1L1 X99209_at X99209 PASS 9 20.78 PASS 13 9 16.08 1.29 1.29 **arginine methyltransferase** RPL10 HG4542-HT4 HG4542-HT PASS 9 184.78 PASS 13 9 143.08 1.29 1.29 28SRNA5 AFFX-M2783 AFFX-M27 PASS 7 8.71 PASS 8 7 6.57 1.29 1.29 YWHA X56468_at X56468 PASS 9 23.33 PASS 13 9 18.08 1.29 1.29 14.3.3 protein ACADM M91432_at M91432 PASS 8 7.50 PASS 11 8 5.82 1.29 1.29 ACADM 1p31 acyl-Coenzyme A acyl-Coenzyme A dehydrogenase, C-4 to C-12 dehydrogenase, C-4 to C-12 straight chain straight chain FMR1 U25165_at U25165 PASS 7 11.00 PASS 13 7 8.54 1.29 1.29 FXR1 3q28 FXR1 fragile X mental retardation, autosomal homolog 1 HMG17_rna1 X13546_rna1 X13546 PASS 9 40.22 PASS 13 9 31.23 1.29 1.29 HMG17 1p36.1-p35 put HMG-17 protein high-mobility group (nonhistone chromosomal) protein 17 K6_VAV1 D25304_at D25304 PASS 9 16.11 PASS 13 9 12.54 1.28 1.28 KIAA0006 PAK-interacting exchange factor alpha SNRPD2 U15008_at U15008 PASS 9 140.33 PASS 13 9 109.23 1.28 1.28 SNRPD2 small nuclear ribonucleo- small nuclear ribonucleo- protein D2 polypeptide protein D2 polypeptide (16.5 kD) (16.5 kD) COX5A M22760_at M22760 PASS 9 16.89 PASS 13 9 13.15 1.28 1.28 COX5A 15q25 cytochrome c oxidase cytochrome c oxidase subunit Va subunit Va VRK1 AB000449_at AB000449 PASS 7 7.57 PASS 10 7 5.90 1.28 1.28 VRK1 14q32 vaccinia related kinase 1 vaccinia related kinase 1 M31516_s_at M31516_s_at M31516 PASS 5 6.20 PASS 12 5 4.83 1.28 1.28 DAF 1q32 decay-accelerating factor decay accelerating factor for complement (CD55, Cromer blood group system) TRPOSL M23161_at M23161 PASS 7 6.29 PASS 11 7 4.91 1.28 1.28 PSMC5 L38810_at L38810 PASS 9 14.67 PASS 11 9 11.45 1.28 1.28 PSMC5 17q23-q25 proteasome (prosome, proteasome (prosome, macropain) 26S subunit, macropain) 26S subunit, ATPase, 5 ATPase, 5 UROD M14016_at M14016 PASS 7 7.86 PASS 7 7 6.14 1.28 1.28 UROD 1p34 uroporphyrinogen uroporphyrinogen decarboxylase decarboxylase POLR2 HG2274-HT2 HG2274-HT PASS 6 10.33 PASS 12 6 8.08 1.28 1.28 M96954_s_at M96954_s_at M96954 PASS 9 7.67 PASS 13 9 6.00 1.28 1.28 Nuclelysin TIAR

TRP185 U38847_at U38847 PASS 5 6.20 PASS 7 5 4.86 1.28 1.28 TRP-185 TAR RNA loop binding TRP-185 protein; GCNT1 U77413_at U77413 PASS 5 7.40 PASS 10 5 5.80 1.28 1.28 OGT O-GlcNAc transferase O-linked N-acetyl- (uridine diphospho-N- glucosamine (GlcNAc) acetylglucosamine:poly- transferase (UDP-N- peptide beta-N-acetyl- acetylglucosamine:poly- glucosaminyl transferase) peptide-N-acetyl- glucosaminyl transferase) RAN HG1112-HT1 HG1112-HT PASS 9 21.44 PASS 13 9 16.85 1.27 1.27 INDPOLABP U33818_at U33818 PASS 8 14.88 PASS 13 8 11.69 1.27 1.27 IPABP inducible poly(A)-binding inducible poly(A)-binding protein protein DPM1 AF007875_at AF007875 PASS 8 8.38 PASS 12 8 6.58 1.27 1.27 DPM1 dolichyl-phosphate dolichyl-phosphate mannosyltransferase poly- mannosyltransferase poly- peptide 1, catalytic subunit peptide 1, catalytic subunit TCP3 M31523.sub.'at M31523 PASS 9 6.89 PASS 12 9 5.42 1.27 1.27 TCF3 19 transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) Z26491_s_at Z26491_s_at Z26491 PASS 9 13.89 PASS 13 9 10.92 1.27 1.27 catechol O-methyl- transferase HNRNPCL M94630_at M94630 PASS 9 27.56 PASS 13 9 21.69 1.27 1.27 HNRPD 4q21 heterogeneous nuclear heterogeneous nuclear ribonucleoprotein D ribonucleoprotein D K212_COSC D86967_at D86967 PASS 7 11.43 PASS 12 7 9.00 1.27 1.27 KIAA0212 KIAA0212 gene product EIF2A U26032_at U26032 PASS 5 5.80 PASS 7 5 4.57 1.27 1.27 TGFBR2 D50683_at D50683 PASS 9 24.00 PASS 13 9 18.92 1.27 1.27 TGFBR2 3p22 transforming growth factor, transforming growth factor, beta receptor II (70-80 kD) beta receptor II (70-80 kD) PPP2R2A M64929_at M64929 PASS 7 7.29 PASS 8 7 5.75 1.27 1.27 PPP2R2A protein phosphatase 2 protein phosphatase 2 (formerly 2A), regulatory (formerly 2A), regulatory subunit B (PR 52), alpha subunit B (PR 52), alpha isoform isoform GPRK5 L15388_at L15388 PASS 6 6.33 PASS 7 6 5.00 1.27 1.27 GPRK5 10q24-qter G protein-coupled G protein-coupled receptor kinase receptor kinase PPP3CB2 M29551_at M29551 PASS 5 7.60 PASS 9 5 6.00 1.27 1.27 calcineurin A2 HG3484-HT3 HG3484-HT3 HG3484-HT PASS 7 8.86 PASS 12 7 7.00 1.27 1.27 CCNH U11791_at U11791 PASS 7 6.43 PASS 12 7 5.08 1.26 1.26 CCNH 5q13.3-q14 cyclin H cyclin H H2B_rna2 X57985_rna2 X57985 PASS 9 9.11 PASS 13 9 7.23 1.26 1.26 H2AFQ 1q21-q23 histone H2A H2A histone family, member Q NFKB1 M58603_at M58603 PASS 6 16.17 PASS 12 6 12.83 1.26 1.26 NFKB1 4q24 nuclear factor kappa-B nuclear factor of kappa DNA binding subunit light polypeptide gene enhancer in B-cells 1 (p105) G22P1 J04611_at J04611 PASS 9 23.44 PASS 13 9 18.62 1.26 1.26 G22P1 22q11-q13 thyroid autoantigen 70 kD thyroid autoantigen 70 kD (Ku antigen) (Ku antigen) RABGGTB X98001_at X98001 PASS 6 6.67 PASS 10 6 5.30 1.26 1.26 RABGGTB 1p31-p22 Rab geranylgeranyl- Rab geranylgeranyl- transferase, beta subunit transferase, beta subunit ECH1 U16660_at U16660 PASS 7 20.57 PASS 13 7 16.38 1.26 1.26 ECH1 19q13.1 enoyl Coenzyme A enoyl Coenzyme A hydratase 1, peroximal hydratase 1, peroximal K276_HYPLK D87466_at D87466 PASS 7 5.71 PASS 9 7 4.56 1.25 1.25 KIAA0276 Similar to S. cerevisiae hypothetical protein L3111 (S59316) K78_RAD21 D38551_at D38551 PASS 8 10.63 PASS 12 8 8.50 1.25 1.25 RAD21 RAD21 (S. pombe) homolog ECGF1 M31210_at M31210 PASS 8 6.38 PASS 10 8 5.10 1.25 1.25 EDG1 1pter-qter endothelial differentiation, endothelial differentiation, sphingolipid G-protein- sphingolipid G-protein- coupled receptor, 1 coupled receptor, 1 M58525_s_at M58525_s_at M58525 PASS 5 10.40 PASS 12 5 8.33 1.25 1.25 COMT 22q11.21- catechol-O-methyl- catechol-O-methyl- transferase transferase HG2639-HT2 HG2639-HT2 HG2639-HT PASS 9 11.89 PASS 13 9 95.4 1.25 1.25 ZNF43_f X59244_f_at X59244 PASS 5 5.60 PASS 10 5 4.50 1.24 1.24 ZNF43 19p13.1-p12 zinc finger protein 43 zinc finger protein 43 (HTF6) (HTF6) D79984_s_at D79984_s_at D79984 PASS 5 6.40 PASS 7 5 5.14 1.24 1.24 KIAA0162 similar to emb-5 protein of C. elegans. MIF_rna1 L19686_rna1 L19686 PASS 9

43.33 PASS 13 9 34.85 1.24 1.24 MIF 22q11.2 macrophage migration macrophage migration inhibitory factor (glcosyla- inhibitory factor (glcosyla-tion-inhibiting factor) tion-inhibiting factor) CBF M37197_at M37197 PASS 8 6.75 PASS 7 8 5.43 1.24 1.24 CEBP CCAAT-box-binding factor M90391_s_at M90391_s_at M90391 PASS 7 7.71 PASS 9 7 6.22 1.24 1.24 IL16 interleukin 16 (lymphocyte interleukin 16 (lymphocyte chemoattractant factor) chemoattractant factor) K29 D21852_at D21852 PASS 9 7.33 PASS 12 9 5.92 1.24 1.24 KIAA0029 CTSS M90696_at M90696 PASS 8 12.38 PASS 11 8 10.00 1.24 1.24 CTSS 1q21 cathepsin S cathepsin S X15673_s_at X15673_s_at X15673 PASS 5 9.40 PASS 10 5 7.60 1.24 1.24 ERH D85758_at D85758 PASS 7 21.86 PASS 13 7 17.69 1.24 1.24 ERH 7q34 enhancer of rudimentary enhancer of rudimentary (Drosophila) homolog (Drosophila) homolog HUM31 U30521_at U30521 PASS 5 6.00 PASS 7 5 4.86 1.24 1.24 P311 P311 protein P311 protein K244_TCEA D87685_at D87685 PASS 8 5.63 PASS 9 8 4.56 1.23 1.23 KIAA0244 similar to human transcription factor TFHS (S34159). PSM1131 D88378_at D88378 PASS 6 6.00 PASS 8 6 4.88 1.23 1.23 proteasome inhibitor hP131 subunit SRI M32886_at M32886 PASS 8 7.00 PASS 13 8 5.69 1.23 1.23 SR1 7 sorcin sorcin PRKAR1A M33336_at M33336 PASS 7 25.71 PASS 13 7 20.92 1.23 1.23 PRKAR1A 17q23-q24 protein kinase, cAMP- protein kinase, cAMP- dependent, regulatory, type dependent, regulatory, type I, alpha (tissue specific 1, alpha (tissue specific extingisher 1) extinguisher 1) AMD1 M21154_at M21154 PASS 8 8.50 PASS 12 8 6.92 1.23 1.23 AMD1 6q21-q22

PGPUB-DOCUMENT-NUMBER: 20030148316

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030148316 A1

TITLE: Methods and compositions relating to plasmacytoid dendritic cells

PUBLICATION-DATE: August 7, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 212133

DATE FILED: August 1, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60309260 20010801 US

US-CL-CURRENT: 435/6, 435/372 , 435/7.21

ABSTRACT:

The invention provides methods and compositions relating to a dendritic cell expression database.

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application filed Aug. 1, 2001, entitled "METHODS AND COMPOSITIONS RELATING TO PLASMACYTOID DENDRITIC CELLS", Serial No. 60/309,260, the contents of which are incorporated by reference herein in their entirety.

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Summary of Invention - Table CWU - BSTL (3):

3TABLE 2a Top 125 positively upmodulated genes by CpG-DNA (2 hours) in human pDC Rank Sort score Accession Gene Name, function 1 246.12 X02956 receptor, soluble, IFN-1, IFNa-05 2 228.66 V00551 receptor, soluble, IFN-1, IFNa-10 3 193.06 V00535 receptor, soluble, IFN-1, IFNb-01 4 189.71 X58822 receptor, soluble, IFN-1, IFN-omega-1 5 186.11 M27318 receptor, soluble, IFN-1, IFNa-04b 6 185.65 J00210 receptor, soluble, IFN-1, IFNa-01/13 7 184.15 V00540 receptor, soluble, IFN-1, IFNa-21 8 175.4 V00542 receptor,

soluble, IFN-1, IFNa-14 9 170.84 V00541 receptor, soluble, IFN-1, IFNa-05 frag 10 168.56 M28585 receptor, soluble, IFN-1, IFNa-16 11 152.77 X02958 receptor, soluble, IFN-1, IFNa-06 12 149.33 J00207 receptor, soluble, IFN-1, IFNa-02 13 81.36 AF030514 receptor, soluble, chemokine, cxcl-11, I-TAC 14 80.61 M55067 miscellaneous, p47-phox, neutrophil nadph oxidase factor-1 15 79.22 U20982 receptor, growth factor, IGF-1, IGFBP4, functionnal antagonist of IGF1 16 74.55 M62403 receptor, growth factor, IGF-1, IGFBP4, functionalantagonist of IGF1 17 73.78 X72755 receptor, soluble, chemokine, cxcl-09, Mig 18 69.56 U04636 enzyme, COX-2, prostaglandin-endoperoxide synthase 2 19 67.61 J00207 receptor, soluble, IFN-1, IFNa-02 20 55.58 U83981 apoptosis, MYD116, GADD34 21 53.18 U27467 apoptosis, BFL-1, retards apoptosis induced by il-3deprivation 22 46.82 M21121 receptor, soluble, chemokine, ccl-05 RANTES 23 44.72 J04130 receptor, soluble, chemokine, ccl-04, MIP-1B 24 41.85 U57646 transcription, zinc finger, CSRP2, cytoskeletal remodeling? 25 37.04 U12767 transcription, nuclear receptor, orphan, MINOR 26 34.98 S79639 housekeeping, EXT-1, golgi, synthesis of heparan sulfate 27 32.89 S79639 housekeeping, EXT-1, golgi, synthesis of heparan sulfate 28 32.07 M16441 receptor, soluble, cytokine, TNFB 29 31.41 D12614 receptor, soluble, cytokine, TNFB 30 31.16 X02530 receptor, soluble, chemokine, cxcl-10, IP-10, IFN responsive 31 30.53 U03398 surface marker, 4-1BB ligand, CD137 interaction, costimulation 32 29.69 X60592 surface marker, CD040, signaling 33 29.21 AI865431 surface marker, CD040, frag? 34 27.32 X04430 receptor, soluble, cytokine, IL-06, precursor, IFN, IFNb2a 35 26.29 AF078096 transcription, FXC1, forkhead box protein c1 36 26.11 M21121 receptor, soluble, chemokine, ccl-05, RANTES 37 26.04 M16441 receptor, soluble, cytokine, TNFB 38 25.12 U19261 signaling, TRAF-1, TNF receptor-associated factor 1 39 24.78 U12767 transcription, nuclear receptor, orphan, MINOR 40 24.42 L31584 receptor, surface, chemokine, ccr-07, EBI-1 41 23.32 D90144 receptor, soluble, chemokine, CCL-03, MIP-1A 42 23.23 AJ225089 enzyme, OASL, 2'-5'oligoadenylate synthetase-like 43 21.44 U19261 signaling, TRAF1 44 21.13 D13891 transcription, HLH, inhibitor of DNA binding 2 45 20.93 D78579 transcription, nuclear receptor, orphan, MINOR 46 20.27 X02910 receptor, soluble, cytokine, TNFA 47 17.97 AF002986 receptor, surface, H963, platelet activating receptor homolog 48 17.47 M36820 receptor, soluble, chemokine, cxcl-02, Mip2a, GRObeta 49 17.21 M14660 miscellaneous, IFN, GARG-39, IFIT2 50 16.78 D14497 kinase, MAP3K8, mitogen-activated protein kinase kinase kinase 8, cot 51 15.83 AF077346 IL-18RAP, interleukin 18 receptor accessory protein 52 15.22 M14660 miscellaneous, IFN, GARG-39, IFIT2 53 15.11 X75042 transcription, NF-kB, rel, v-rel 54 14.87 Z30644 channel, clc-k2, chloride channel protein clc-kb 55 14.56 D78579 transcription, nuclear receptor, orphan, MINOR 56 14.55 L11329 phosphatase, DUS2, dual specificity protein phosphatase 2 57 12.47 J05008 receptor, ENDOTHELIN-1 PRECURSOR (ET-1), vasoconstriction 58 12.31 AF026939 IFT4, Cig-49, interferon-induced protein with tetratricopeptide repeats 4 59 12.23 L19871 ATF3, CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR 60
11.95 AF005775 apoptosis, CFLA, cellular flice-like inhibitory protein (c-flip) 61 11.48 AB002344 unknown 62 11.18 M56803 transcription, NF-kB, p105, nuclear factor nf-kappa-b p105 subunit 63 11.1 M29039 transcription, JUN-B, transcription factor jun-b 64 10.93 S76638 transcription, NF-kB, p50, (p49/p100) 65 10.85 M69043 transcription, NF-kB, IkB, MAD 66 10.56 M15330 receptor, soluble, cytokine, IL-01B, IL-1 beta 67 10.55 X61498 transcription; NF-kB, nuclear factor nf-kappa-b p100 subunit 68 10.47 X58072 transcription, GATA-3 ENPP2, ectonucleotide pyrophosphatase/phosphodiesterase 2 69 10.21

D45421 (autotaxin) 70 10.17 Z14138 **transcription, MAP3K8, mitogen-activated** protein kinase kinase kinase 8 71 9.93 U40992 heat shock, DNAJB4, DnaJ (Hsp40) homolog, subfamily B, member 4 72 9.83 U70426 signaling, G protein, RGSG16, regulator of g-protein signaling 16 (rgs16) 73 9.73 S76638 transcription, NF-kB, p50, (p49/p100) 74 9.67 AB007858 enzyme, 5'cap guanine-N-7 **methyltransferase** af067791 75 9.65 U45878 apoptosis, BIR3, inhibitor, binds Traf-1 and 2 76 9.51 S59049 signalling, G protein, RGS1, regulator of g-protein signaling 1 77 9.46 X07743 signalling, pleckstrin, p47 78 9.21 D13891 HLH, inhibitor of DNA binding 2 79 9.09 L40387 OASL, 2'-5'oligoadenylate synthetase-like, nuclear receptor, TRIP14 80 8.89 X89750 TGIF, TG-interacting factor, inhibitors retinoid x receptor (rxr) 81 8.78 AB004904 transcription, STAT, SOC53, STAT induced STAT inhibitor 3 82 8.74 Z22576 surface marker, CD069, C-type lectin, signaling 83 8.64 U77735 kinase, pim-2, (serine threonine kinase) 84 8.21 AF078077 apoptosis, GADD45B, MyD118 85 7.48 M58603 transcription, NF-kB, p105, nuclear factor nf-kappa-b p105 subunit 86 7.43 M36067 replication, DNA ligase 1, ATP dependent 87 7.33 M16750 signalling, kinase, pim-1 88 7.25 AB002344 unknown 89 7.2 L28175 receptor, PE24 prostaglandin E receptor 4 (subtype EP4) 90 7.11 U49187 miscellaneous 91 6.97 M24398 transcription, parathymosin, inhibitor 92 6.57 AF005775 apoptosis, CFLA 93 6.25 U40992 heat shock, DNAJB4, DnaJ (Hsp40) homolog, subfamily B, member 4 94 6.14 L25124 receptor, PE24 prostaglandin E receptor 4 (subtype EP4) nuclear receptor, TR3 (NGFI-B, Nur77), steroid/thyroid receptor 95 6.13 L13740 superfamily 96 6.12 Z11697 surface marker, CD083, blast marker for DC 97 6.11 AF001434 receptor, EHD1, participating in clathrin-coated pit-mediated endocytosis 98 6.01 AF117829 signalling, RIPK2, receptor-interacting serine-threonine kinase 2 99 6 Y11306 TCF-4, TCF7L2 transcription factor 7-like 2 (T-cell specific, HMG-box) 100 5.98 S76792 surface marker, CD134, OX40 101 5.98 U91512 surface marker, adhesion, ninjurin (nerve injury-induced protein 1) 102 5.95 AB000734 signalling, SSI1, STAT-induced STAT inhibitor-1, JAK binding protein 103 5.86 D64142 replication, transcription, histone, H1Fx 104 5.74 M92357 TNFAIP2 tumor necrosis factor alpha-induced protein 2, RA induced, B94 105 5.72 Z23115 apoptosis, bcl-xL, dominant regulator of apoptotic cell death neuromedin B, Bombesin-like peptides, bombesin/neuromedin 106 5.68 AI985272 b/ranatensin 107 5.63 M58603 transcription, NF-kB, p105, nuclear factor nf-kappa-b p105 subunit 108 5.62 M54915 signalling, kinase, pim-1 109 5.47 Z23115 apoptosis, bcl-xL, dominant regulator of apoptotic cell death transcription, nuclear, CREM, cAMP responsive element modulator, fos 110 5.45 S68134 jun transcription, RNA pol, RPC62 polymerase (RNA) III (DNA directed) 111 5.43 U93867 (62 kD) 112 5.4 AI971169 unknown 113 5.38 AB006624 unknown 114 5.27 W27419 NT_004511.4.vertline.Hs1_4668 Homo sapiens 115 5.19 M24283 surface marker, CD054, ICAM-1 116 5.05 U00672 receptor, surface, cytokine, IL-10R 117 4.99 U83115 miscellaneous, AIM1, absent in melanoma 1 118 4.94 M11186 receptor, oxytocin, prepro- (neurophysin I), contraction signalling, CHML, Rab escort protein-2, activating 119 4.85 X64728 geranylgeranyltransferase A 120 4.69 W28729 unknown 121 4.63 AI138605 miscellaneous, DKFZP566A1524 hypothetical protein DKFZp566A1524 122 4.62 AF030107 signalling, G protein, RGS13, regulator of G-protein signalling 13 123 4.46 X70326 surface marker, adhesion, MacMarcks, integrin activation transcription, nuclear, CREM, cAMP responsive element modulator, fos 124 4.43 S68134 jun 125 4.41 U03057 structural protein, fascin, actin bundling protein

US-PAT-NO: 6610504

DOCUMENT-IDENTIFIER: US 6610504 B1

TITLE: Methods of determining SAM-dependent methyltransferase activity using a mutant SAH hydrolase

DATE-ISSUED: August 26, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Yuan; Chong-Sheng	San Diego	CA	N/A	N/A

APPL-NO: 09/ 546013

DATE FILED: April 10, 2000

PARENT-CASE:

RELATED APPLICATIONS

This application is related to U.S. application Ser. No. 09/347,878 to Chong-Shen Yuan, filed Jul. 6, 1999, now U.S. Pat. No. 6,376,210 entitled "COMPOSITIONS AND METHODS FOR ASSAYING ANALYTES" and U.S. application Ser. No. 09/457,205 to Chong-Shen Yuan, filed Dec. 6, 1999, entitled "COMPOSITIONS AND METHODS FOR ASSAYING ANALYTES." U.S. application Ser. No. 09/457,205 is a continuation-in-part application of U.S. patent application Ser. No. 09/347,878, filed Jul. 6, 1999, now U.S. Pat. No. 6,376,210. The contents of each of these applications is incorporated herein in its entirety.

US-CL-CURRENT: 435/15, 435/18

ABSTRACT:

The present invention relates to compositions and methods for assaying the activity of methyltransferases, such as S-adenosylmethionine (SAM)-dependent methyltransferases. The methods can be used for screening for modulators of such methyltransferases, for identifying substrates and for diagnostics. The methods are amenable for use in high throughput formats. Kits for performing the methods are also provided.

17 Claims, 0 Drawing figures

Exemplary Claim Number: 1

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Brief Summary Text - BSTX (5):

Methyltransferase, including SAM-dependent **methyltransferase,** catalyzed abnormal methylation has been linked to pathological conditions (see, e.g., U.S. Pat. No. 5,876,996). For example, covalent modification of cellular substrates with methyl groups has been implicated in the pathology of cancer and other diseases (Gloria, et al., Cancer, 78:2300-2306 (1996)). Cytosine hypermethylation of eukaryotic DNA prevents **transcriptional activation** (Turker and Bestor, Mutat. Res., 386:119-130 (1997)). N.sup.6 -methyladenosine is found at internal positions of mRNA in higher eukaryotes (Bokar, et al., J. Biol. Chem., 269:17697-17704 (1994)). Hypermethylated viral DNA is transcribed at higher rates than hypo- or hemimethylated DNA in infected cells (Willis, et al. Cell. Biophys., 15:97-111 (1989)).

US-PAT-NO: 6607882

DOCUMENT-IDENTIFIER: US 6607882 B1

TITLE: Regulation of endogenous gene expression in cells using zinc finger proteins

DATE-ISSUED: August 19, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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Case; Casey C.	San Mateo	CA	N/A	N/A
Eisenberg; Stephen P.	Boulder	CO	N/A	N/A
Jarvis; Eric E.	Boulder	CO	N/A	N/A
Spratt; Sharon K.	Vacaville	CA	N/A	N/A

APPL-NO: 09/ 478681

DATE FILED: January 6, 2000

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is a continuation-in-part of and claims the benefit of co-pending U.S. Ser. No. 09/229,037, filed Jan. 12, 1999.

US-CL-CURRENT: 435/6, 435/320.1 , 435/455 , 435/468 , 536/23.1 , 536/23.4 , 536/24.1

ABSTRACT:

The present invention provides methods for modulating expression of endogenous cellular genes using recombinant zinc finger proteins.

32 Claims, 16 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 11

---------- KWIC ---------

Detailed Description Text - DETX (31):

A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription

factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detailed Description Text - DETX (81):

Common regulatory domains for addition to the ZFP include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.